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Yang et al.

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(54) **BIOCATALYSTS WITH ENHANCED
INHIBITOR TOLERANCE**

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(58) **Field of Classification Search**

CPC combination set(s) only.

See application file for complete search history.

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(57) **ABSTRACT**

Disclosed herein are biocatalysts for the production of biofu-
els, including microorganisms that contain genetic modifica-
tions conferring tolerance to growth and fermentation inhibi-
tors found in many cellulosic feedstocks. Methods of
converting cellulose-containing materials to fuels and chemi-
cals, as well as methods of fermenting sugars to fuels and
chemicals, using these biocatalysts are also disclosed.

18 Claims, 15 Drawing Sheets

Figure 1

A. SEQ ID NO:1

ATGACTTTTCCCAATCAAGGCTGAGAAAGGACTGCGTTATTAAATTTATCCCTGTCTATCT
ATCCGGATTATCAATCCTGGCTCTATTTATTATTGCCGTCAGTCATGTTTCTGTGGGTGGC
CGATCTTGTGCTTATGCTGATTGTTATCCTTTGGGGATGGTGGTTTAAAAATATTTCCGAA
GCGTCTACCCCTTCCCTGAAAGTAAAAGCGGAAATAGCCTTACGGATCCTGCCTATCCTTT
TTCTCAAGCGACAGCGGCAGATATTATTATAGCTATGGATGAACCAGCTTTACTGGTCAATC
AGGGTCAAGTTGAAGTGGCTAATCGTGCCGCTGAAAATTTGTTAGGGATGCATATCGAAGGA
GGCGACATCAGAATGGCTATTCGCCATCCTGCTGCTATCCGTCCTTTTAACCGAGCCGCTTGA
TAATATGACTCCTGTTTTACTTGCCGGATTGGGAGGCGTTAATCGTCGCTGGGAATTATACG
CTTATCCTTTGAACGAAGAACAACGGCTCATTTTGTGCGCGATCAAAGTACGGCTCATTTA
ACGGAACAGGTTAGAATAGACTTTGTTGCGAATACTAGTCACGAATTACGGACACCGCTCGC
GACTTTAAGCGGGTTTATTGAGACATTAGAAGATGATGATGTCATTAAAGAGCGCGATACGC
GTCATCATTTTTTGTCTATTATGGCGCGTGAAGCCAAAAGAATGCAAAATTTGGTTGATGAC
TTGATGTCTCTTCTCGGATTGAAGCCGAAAATTTTCATTACCCCATGATATTGTTTCATAT
GTCGCCTGTGGTTGAAGAGGTCGTGTCTAATATTCAGGCATCGGGACAGGCAAAAGCCACCC
AAATCACACTCGAAAATCATTTGTCCAGTGATAGCCTACAGGGTGACCGCGCCGAGTTAACG
CAGCTCCTTTATAACATTATCGGCAATGCCTTAAAATATGGTCGTAAAGATGGAATAATTAA
AGTCGCGCTCGATAATACTGACGATCATAGAATAAAATTAGCTATTGCAGATGAAGGCGATG
GTATTCCGTTTCATCATATCCCGCGCCTAACGGAACGCTTCTATCGGGTGGATAACAGCCGT
AGTCGCGCTTTAGGGGGAACAGGATTGGGGCTAGCCATAGTAAAACAAATCGTCGAGCATCA
TCGCGGAGAATTACTGATAGACAGCCTCCCCGGTAAAGGGACGACGGTAACCGTTTTTCTTGC
CAACGACCGATTTTTTCCCTGAA

B. SEQ ID NO:2

MTFPQSRLRKDCVIKFI PVYLSGLSILALFIIAVSHVSVGWPILSLMLIVILWGWWFKNISE
ASTPFPEKSGNSLTDPAYPFSQATAADII IAMDEPALLVNQGQVEVANRAAENLLGMHIEG
GDIRMAIRHPAAIRLLTEPLDNMTPVLLAGLGGVNRWELYAYPLNEEQRLILLRDQSTAHL
TEQVRIDFVANTSHELRTPLATLSGFIETLEDDVIKERDTRHHFLSIMAREAKRMQNLVDD
LMSLSRIEAGKFS LPHDIVHMSPVVEEVVSNIQASGQAKATQITLENHLS SDSLQGDRAELT
QLLYNIIGNALKYGRKDGI IKVALDNTDDHRIKLAI ADEGDGIPFHHPRLTERFYRVDNSR
SRALGGTGLGLAIVKQIVEHHRGELLIDSLPGKGT TVTVFLPTTDFPE

Figure 2

A. SEQ ID NO:3

ATGGATATCCGTATTTCCGGCCATCAGATTGATACAGGCGCGGCTTTAAGAGAATATGTCAA
TGACCATCTTAGCCAGATCGTCAGCAAATATTTCCCAAATGCCTAAGCGCCTCTGTCACTT
TCGGTAATCGTCGCCACGCTATTATTTCTGCGATATTATTATCCATGCCATGCGGGATATT
ATTCTGAAAGCAGGCGGCATAGACAAAGACGCCCATGCCGCTTTCGATCAGGCCGCCGCCAA
GATTGAAAAACAATTACGGCGACATCACCGACGTTTACAGACCCGCGTCCAGCAAATAACGC
CTTCTATTGATGAAGCCGCTATCGCCCTTACGGAGGCAACAGCCAAGGCGGATCAGGATAAC
GCGCATTATACGGTCTTTGACATTGAAGAGGATGAAAAAGAGCAAGGCGATCATCCTCCCGT
CATTGCCGAAATGCAGGTTGATATTCCAACAGCCAGCGTTTCCGATGCTGTTTTGATGCTCG
ATCTTCGCAACACGACGGCTTTGCTCTTCGTGAACAGCAAATCGGGTCATCATAATATGGTT
TATCGTCGGGTAGATGGTACCATCGGTTGGGTTGAGCCGCGA

B. SEQ ID NO:4

MDIRISGHQIDTGAALREYVNDHLSQIVSKYFPKCLSASVTFGNRRHAIISCDIIHAMRDI
ILKAGGIDKDAHAAFQAAAKIEKQLRRHHRRLQTRVQQNTPSIDEAAIALTEATAKADQDN
AHYTVFDIEEDEKEQGDHPPVIAEMQVDIPTASVSDAVLMLDLRNTTALLFVNSKSGHHNMV
YRRVDGTIGWVEPR

Figure 3

A. SEQ ID NO:5

ATGCCTAATGCAGAGTTTGATTTTCAGGCCTATGTTTCCGAATAAAAAGACGCCGTTGTTAGA
CAAGATCAAGACACCGGCAGAATTGCGTCAATTAGATCGCAACAGCCTCCGGCAATTGGCGG
ATGAATTACGGAAAGAGACCATCTCGGCAGTGGGTGTGACCGGCGGACATCTCGGTTCCGGT
CTGGGGGTTATCGAATTAACGGTAGCTCTTCATTATGTTTTCAACACGCCCAAAGACGCTTT
GGTCTGGGATGTTGGGCATCAAACCTATCCTCACAAGATTTTAACAGGTCGCCGTGATCGTA
TTCGGACATTGCGGCAACGTGACGGCTTATCGGGCTTTACGCAGCGCGCGGAGAGCGAATAT
GACGCTTTTGGAGCAGCGCATAGTTCGACTTCTATTTCTGCGGCGCTCGGCTTTGCGATGGC
CAGCAAATTATCCGACAGCGACGACAAAGCGGTTGCGATTATCGGTGATGGCTCGATGACGG
CAGGCATGGCTTATGAAGCCATGAATAACGCCAAGGCGGGTAAGCGCCTGATTGTCATT
TTGAATGACAATGAAATGTCGATTTACCGCCGGTGGGTGCCTTATCGTCTTATTTGAGCCG
CCTGATTTCTCACGGCCTTTTCATGAATTTGCGCGATATCATGCGCGGTGTTGTCAACCGGA
TGCCAAAAGGCTTGGCAACGGCTGCCCGCAAGGCTGATGAATATGCGCGTGGTATGGCAACC
GGTGGCACCTTCTTTGAAGAGCTGGGCTTTTACTATGTTGGCCCCGTAGATGGTCATAATTT
AGATCAGCTCATTCCGGTTTTTGAAAATGTCCGCGATGCCAAGGACGGCCCCATTTTGGTGC
ATGTCGTCACCCGCAAAGGCCAAGGCTATGCTCCGGCTGAAGCGGCCAAGGACAAATATCAC
GCCGTGCAGCGCTTGGATGTGGTTTTCCGGCAAGCAGGCGAAAGCGCCCCCAGGGCCTCCCAG
CTATACCTCTGTTTTCTCGGAACAGCTGATCAAGGAAGCTAAGCAAGACGATAAGATTGTGA
CCATTACGGCAGCTATGCCGACTGGCACC GGCTTGTATCGCTTCCAGCAATATTTTCTGAA
AGAATGTTTGATGTCGGTATTGCCGAACAACATGCCGTAACCTTTGCGGCTGGTTTTGGCGGC
TGCCGGTTACAAGCCTTTCTGTGTCTCTATTTCGACCTTCTTGCAGCGCGGCTATGACCAGT
TAGTGCATGATGTCGCTATCCAGAATTTGCCGGTGCCTTCCCGTCGATCGTGCGGGTCTT
GTCGGTGCCGATGGGGCAACCCATGCGGGTAGCTTCGACCTCGCCTTTATGGTTAATCTACC
GAATATGGTTCGTGATGGCGCCTTCCGATGAACGGGAATTGGCCAATATGGTGCATAGCATGG
CGCATTATGACCAAGGCCCGATCTCGGTGCGTTATCCGCGTGGTAATGGTGTGGGTGTCTCC
TTGGAAGGCGAAAAGGAAATCTGCCTATCGGGAAAGGTCGCCTGATCCGTGCGGGTAAAAA
GGTTGCTATCCTATCTCTCGGCACTCGATTGGAAGAATCCTTGAAGGCTGCTGATCGGCTTG
ATGCTCAAGGTTTGTGACATCGGTTGCTGATATGCGTTTTTGCTAAGCCCTTGGATGAAGCG
CTGACCCGCCAACTTCTAAAAGCCATCAGGTCATTATTACCATTGAAGAAGGCGCTTTGGG
TGGTTTTGCAACCCAAGTCTGACGATGGCTTCGGATGAAGGCCTGATGGATGACGGATTGA
AAATCCGCACCCTGCGTCTGCCGGATCGGTTCCAGCCGCAAGACAAGCAAGAACGGCAATAT
GCCGAAGCTGGTCTTGATGCTGATGGCATCGTTGCTGCCGTAACGGCTGCATTACAACGGAA
CTCAAAGCCTGTCGAAGTCGTTGAGCTGACTACAAAAGTAACAGAAGATATGACTTTATGA

B. SEQ ID NO:6

MPNAEFDFRPMFPNKKTPLLDKIKTPAELRQLDRNSLRQLADELRKETISAVGVTGGHLGSG
LGVIELTVALHYVFNTPKDALVWDVGHQTYPHKILTGRRDRIRTLRQRDGLSGFTQRAESEY
DAFGAAHSSTSI SAALGFAMASKLSDSDDKAVAI IGDGSMTAGMAYEAMNNAKAAGKRLIVI
LNDNEMSI SPV GALSSYLSRLISSRPFMNL RDIMRGVVNRMPKGLATAARKADEYARGMAT
GGTFFEELGFYYVGPVDGHNLDQLIPVLENVRDAKDGPILVHVVTRKGGYAPAEAAKDKYH
AVQRLDVVSGKQAKAPPGPPSYTSVFSEQLIKEAKQDDKIVTITAAMPTGTGLDRFQQYFPE
RMFDVGIAEQHAVTFAAGLAAAGYKPFCCLYSTFLQRGYDQLVHDVAIQNLPVRFVDRAGL
VGADGATHAGSFDLAFMVNLPNMVVMAPS DERELANMVHSM AHYDQGPISVRYPRGNGVGV
LEGEKEILPIGKRLIRRGKKVAILSLGTRLEESLKAADRLDAQGLSTSVADMRFKPLDEA
LTRQLLQSHQVIITIEEGALGGFATQVLTMASDEGLMDDGLKIRTLRPLPDRFQPQDKQERQY
AEAGLDADGIVA AVT AALQRNSKPVEVVELTTKVTEDMTL

Figure 4

A. SEQ ID NO:7

ATGTTTCCGAATGACAAGACGCCGCTGTTAGACAAGATCAAGACACCGGCAGAATTGCGTCA
ATTAGATCGCAACAGCCTCCGGCAATTGGCGGATGAATTACGAAAGAGACCATCTCGGCAG
TGGGTGTGACCGGCGGACATCTCGGTTCCGGTCTGGGGGTTATCGAATTAACGGTAGCCCTT
CACTATGTTTTCAACACGCCCAAAGACGCTTTAGTCTGGGATGTTGGGCATCAAACCTATCC
TCACAAGATTTTAAACAGGTCGCCGCGATCGTATTCGGACATTGCGGCAACGTGACGGCTTAT
CGGGCTTTACGCAGCGCGCGGAGAGCGAATATGACGCTTTTGGAGCCGCGCATAGTTCGACT
TCTATTTCTGCGGCGCTCGGCTTTGCGATGGCCAGCAAATTATCCGACAGCGACGACAAAGC
GGTTGCGATTATCGGTGATGGCTCGATGACGGCAGGCATGGCTTATGAAGCCATGAATAACG
CCAAGGCGGCGGGTAAGCGCCTGATTGTCATTTTGAATGACAATGAAATGTCGATTTACCG
CCGGTGGGTGCCTTATCGTCTTATTTGAGCCGCTGATTTCCCTCACGGCCTTTCATGAATTT
GCGCGATATCATGCGCGGCGTTGTTAACCGGATGCCAAAAGGCTTGGCAACGGCTGCCCGCA
AGGCTGATGAATATGCGCGTGGTATGGCAACCGGTGGCACCTTCTTTGAAGAGCTGGGCTTT
TACTATGTTGGCCCCGTGGATGGTCATAATTTAGATCAGCTCATTCCAGTTTTAGAAAATGT
CCGCGATGCCAAGGACGGCCCCATTTTGGTGCATGTCGTCACTCGCAAAGGCCAAGGCTATG
CTCCGGCTGAAGCGGCCAAGGACAAATATCACGCCGTGCAGCGCTTGGATGTGGTTTTCCGGT
AAGCAGGCGAAAGCGCCCCGGGACCTCCAGCTATACTCTGTTTTTTTCGGAACAGCTGAT
CAAGGAAGCTAAGCAAGACGATAAGATTGTGACCATTACGGCAGCTATGCCGACTGGCACCG
GTCTTGATCGTTTTTACGCAATATTTTCTGAAAGAATGTTTATGTCGGTATTGCCGAACAA
CATGCCGTAACCTTTGCGGCTGGTTTGGCGGCTGCCGGTTACAAGCCTTTCTGTTGTCTCTA
TTCGACCTTCTTGCAGCGCGGCTATGACCAGTTGGTGCATGATGTCGCTATCCAGAATTTGC
CGGTGCGCTTCCCGTTCGATCGTGCGGGTCTTGTCCGTGCCGATGGGGCAACCCATGCGGGT
AGCTTCGACCTCGCCTTTATGGTTAATCTCCCGAATATGGTTCGTGATGGCGCCTTCCGATGA
ACGGGAATTGGCCAATATGGTGCATAGCATGGCGCATTATGACCAAGGCCGATCTCGGTGC
GTTATCCGCGTGGTAATGGTGTGGGTGTCTCCTTGGAAAGGTGAAAAGGAAATTCTGCCTATC
GGGAAAGGTGCGCTGATCCGTCGCGGTA AAAAGGTTGCTATCCTATCTCTCGGCACTCGATT
GGAAGAATCCTTGAAGGCTGCTGATCGGCTTATGCTCAAGGTTTGTGACATCGGTTGCTG
ATATGCGTTTTTGCTAAGCCCTTGGATGAAGCGCTGACCCGCCAACTTTTGAAGCCATCAG
GTCATTATTACCATTGAAGAAGGCGCTTTGGGTGGTTTTTGCAACCCAAGTCTGACGATGGC
TTCGGATGAAGGCTGATGGATGACGGATTGAAAATCCGCACCCTGCGTCTGCCGGATCGGT
TCCAGCCGCAAGACAAGCAAGAACGGCAATATGCCGAAGCCGGTCTTGATGCTGATGGCATC
GTTGCTGCGGTTATCTCCGCATTGCATCGTAATCTAAACCCGTGGAAGTCGTCGAAATGGC
GAATATGGGTAGCATCGCTCGCGCTTAA

B. SEQ ID NO:8

MFPNDKTPLLDKIKTPAELRQLDRNSLRQLADELRKETISAVGVTGGHLGSGLGVIELTVL
HYVFNTPKDALVWDVGHQTYPHKILTGRRDRI RTL RQRDGLSGFTQRAESEYDAFGAAHSST
SISAALGFAMASKLSDSDDKAVAIIGDGSMTAGMAYEAMNNAKAAGKRLIVILNDNEMSISP
PVGALSSYLSRLISSRPFMNL RDIMRGVVNRMPKGLATAARKADEYARGMATGGTFFEELGF
YYVGPVDGHNLDQLIPVLENVRDAKDGPILVHVVTRKGQGYAPAEAAKDKYHAVQRLDVVSG
KQAKAPPGPPSYTSVFSEQLIKEAKQDDKIVTITAAMPTGTGLDRFQQYFPERMFDVGI AEQ
HAVTFAAGLAAAGYKPFCCLYSTFLQRGYDQLVHDVAIQNLPVRFVAVDRAGLVGADGATHAG
SFDLAFMVNLPNMVVMAPS DERELANMVHSM AHYDQGPISVRYPRGNGVGV SLEGEKEILPI
GKGR LI RRGK KVA ILSLGRLEESLKAADRLDAQGLSTSVADMRF AKPLDEALTRQLL KSHQ
VIITIEEGALGGFATQVLT MASDEGLMDDGLKIRTLRLPDRFQPQDKQERQYAEAGLDADGI
VAAVISALHRNSKPV EVVEMANMGSIARA

Figure 5

A. SEQ ID NO:9

TTGAAACGAAAATTGCTCCAATATCTGTTTTTGCCGGATCAGTCTTGATGATGCTGACGGC
CTGTCACCATCAATCCCAAGAAGCCGAACCGGCATTGCAAGATGTTAGTTTTGTTACCGTAA
AAACGCAGCCTTTGACCGTTCATAGCACCTTACCCGGTCGCACTTCGGCTTATGAGGTGGCG
GAAGTAAGACCTCAGGTAAATGGGGTCGTTTTGGCGCGCTATTTTAAACGAAGGCACGGATGT
CAAAAAGGGCAGCCGCTATTCCTTATCAATCCGGCTCCTTATCAAGCGACTTATGACGTTA
ATAAAGCGCAATTAGCTCATGCTGAAGCGCAAGAGAAAACGGCTGCTGCTAAATTAGAACGC
TATAAGGCTTTGGCTCCGGCGCAGGCGATTAGTCGTCAGGATTATGATGATGCTTTGGCCAC
CGATCGCGCGGCCAAGGCAGATATTGCCAAGCCAAAGCGAATATTGAATTATCGGCTGTTA
ATTTGGGATACACCCGTGTGACCGCGCCTATTACTGGCCGGATCGGGCGCGTTTTGACAACG
GTCGGTGCCTTGGTAACTCGGGGCAAAGTTCGAATATGGCGATTGTGACCCGCCTTGACCC
GATTTATGTCGATGTGAATTTGCCAACAGTCGATTTTTTACGGTTGCGGCGCGAGTTAAAAG
CGGGAACCTTTGAAACGGAACGGCAATGATGCCGAAGTCTCCCTTATTCTCGATGATAATTCG
ACCTATAATCAAAAAGGACGGCTGGCTTTAAGCGAAGTCAGTGCCGACACCCAGACATCGAC
CATTGTTGTTTCGTGCGGTTTTCCCAAATCCTGAACATTTGTTGCTGCCCGGAATGTTTGT
ATGGTCGGATAGAAGAGGGCGTTGATCCGAACGCCTTGTTGGTTCGCAAGAATCCGTTTTTC
CGAAATAACCACGGTGATCCGATGTTATATGTCGTCAATAAAGACGACGTTATTGAAGCACG
CCCGATAAAAACCGGTGAAGCTATCGGAACGCAATGGGCTGTGACATCCGGTTTGCAAAAAG
GCGAACGCGTTTTGGTCTCTGGTCTTCAAAAAGTGAATATCGGCGACAAAGTTCATCCGACA
GAGGCTTCTCTTACCAAAGATGCCTCGCCAGAAAAGAAGGGCGGCAAGGCGTAA

B. SEQ ID NO:10

MKRKIAPISVFAGSVLMMLTACHHQSQEAEPALQDVSFVTVKTQPLTVHSTLPGRTSAYEVA
EVRPQVNGVVLARYFNEGTDVKKGQPLFLINPAPYQATYDVNKAQLAHAEAEQEKTAALKER
YKALAPAQAI SRQDYDDALATDRAAKADIAQAKANIELSAVNLYTRVTAPITGRIGRVLTT
VGALVTSQSSNMAIVTRLDPYVDVNLPTVDFLRLRRELKAGTLKRNGNDAEVSLLDDNS
TYNQKGRLLALSEVSADTQTSTIVVRAVFPNPEHLLLPGMFVYGRIEEGVDPNALLVPQESVF
RNNHGDPMPLYVVKDDVIEARPIKTGEAIGTQWAVTSGLQKGERVLVSGLQKVNIGDKVHPT
EASLTKDASPEKKGGKA

Figure 6

A. SEQ ID NO:11

ATGGCTCGCTATTTTATTGACCGCCCTGTTTTTGGCTTGGGTTATCGGTCTTATCATCATGTTATTGGGTGCCCTGGCAA
TTGTTAAAATGCCTATTGCCAATATCCGAATGTTGCCCTCCGCAGATTGAGATCAGTGTGTCTTATCCGGGGGCGTC
GGCTGAAACGATCAATAATACCGTTGTTCCGGCCTATCTTACAGCAGATGCATGGCATCGATAATCTGGAATATATTTTCG
GCTTCTTCTTTGCATCAGGTCAGATGACGATTGATTTGACCTTTGCACAAGGTACCGATGCCGATATCGCACAGGTGC
AAGTCCAGAATAAATTACAATTAGCGCAGCCTCGTTTGGCGTCCGGATGTGGTCAATCAGGGTATTACGGTTAACCGTTC
TGCCAAAAGTTTTATGATGATTATGTCCTTCATCTCGACCGATGGCAGTATGTCCTATCAGGACATCAACGATTATGTG
GCATCGAATATTGCTGATCCGTTGAGCCGTGTTTCCGGTGTGGCGATTACACTCTGTTCCGTTTTGAATATGCAATGC
GGGTCTGGTTAGATCCAGCAAAGCTCTACAAATATAATTTGACTGTAGCGGATGTCCAATCAGCTATTTCTACCCAGAA
TATTCAGCTTTTCATCCGGTGAATTGGGCGGATTGCCCTGCCGTTTCCAGGGTATTGTTGGATGCGACCATTATTGGCCCG
ACCCGTTTGACCTCGCCTGAAGAATTTAAAAATATTCTGGTCAAGGCTTTGCCGGATGGCGCCCAAATCAAATTGGGTG
ACATCGCTAAAGTAGAGTTGGGCGCGCAAAGCTATAACTTTGACGTGCGCTATAATAACCAGCCGGCTTCGGGTATTGC
GATCAAATTGGCACCGGGGGCGAACCAGCTTCAAAGTGAAGGTTGATCCGTCAGCGTTTGGCCGATTGGAACCTTTC
TTCCCTCATGGTTTGAAGGTCGAATATCCGGTTGATACCAAGCCATTTGTGACGGCTTCTATCCATGAGGTTATTGAAA
CCTTGGTGAAGCTATTGCGCTTGTTCCTTGGTGTGCTGATCTTCTTGCAGAATTTCCGTGCTACCTTGATCCCGAC
GATTGCTGTGCCAGTGGTGTGTTAGGCACCTTTGGTGTGCTTTCTGTTCTTGGTTTTTCAATCAATACTCTGACGATG
TTGGCAATGGTCTTGGCTGTTGGCTTGTGGTTCGATGATGCCATCGTCGTTGTTGAAAAATGTCGAACGTTTGATGCGAG
ATGAAAAGCTGCCCCGAAAAGAGGCGGCGAAGCGCTCGATGGATGAAATTTCTGGTGTCTTGATCCGGTATCGTCTTGGT
CTTGTCCGGCCGTGTTCTTGCTATGGCGGCTTTTCCAGGGTCAACGGGCGTTATCTATCGCCAATTTCTCGATTACGATT
GTGGTGGCGATGGGGCTGTCTGTCTTGTGGCGATGATTATGACGCCAGCCCTTTGCGCAACGATGTTAAAGCCGATTG
ACCATGACCAAGCCGATAAAAAGCCGGGTATCTTTGGTTCGCTTGGCGAATGGCTTTAACCGTGTCTTTGACCGATTGAA
TAATGGTTATTTGGGTGGTGTCTTGGTTGTTAGGACGTTCCGTCAAAGGCGGCATTGCCTTTTGTATCATTGTTTTT
GCCGTTGGTTATTTACTCGCTTGCCAACCGGATTTTCCGGATGAAGATCAGGGTGAATTTATTGGTCAGGTGA
CCTTACCAGCCGGGGCGAACCAAGAACAACCGTCCGGAAGCGGTGCGCAAGGTTAATGATTATCTTCTGTCCGCAGAGAA
AGACAGTGTATATCTGTGATGACGGTTAGCGTTTTAACTTTGGTGGTTCAGGGACAAAATGCCGGTTCTTTCTTCGTT
CGTTTTGAAACCTTGGGATCAGCGTCCGAAAGCCTCGCAAAGTCTTCCGGCTTGGCAATGCCGACGATGATGCATTTTT
GGGGTGTCCGTCATCGATGACTTTTGCCTTAAATATGCCTGCTGTCCGCGACTTGGGTAATGCCACCGTTTTGACCT
TGAAGTGAAGATCGCGGTCATATCGGTCATGCAAAATTCCTTGAAGCCCGTAACATGTTATTGGCTTTGGCCTCGAAA
GATCCCGCTTAAAGTGGTGTCCGTCCGAATGGTATGGAAGATGCCCTCAATATCATTGACCGTTGATTACGGCAAAG
CTGTTATGATGGGATTGACCCCAAATGATGTGAATGTGGCCTTGCAGGGGTCTTTGGGGTCGATTTACGTCAATCAGTT
TATGCGGGATGACCGTGTGAAGCAGGTCTATTTAATGGGGCACCGGAAGCGGTATGCTGCCTTCCGATTTTTCCAAA
TGGTATCTGCGGAATAATGTCCGCACGATGGTTCCCTTTAGCGCCTTTATGACAGGAACATGGCAAACGGGCCCTCAGA
AAGTCAAAAATTATAACGGCTATAATCTTTGCAAAATATGGGCGCGCCTGCACCGGGACATAGTTCGGGTGAAGCCAT
TCAGGCGATGACCGAGATCGTTCATAAATGCCAGCTGGTGTGGGCATGAATGGACAGGGTTATCTTTGAAGAGCAG
GCGGCCGTTCCGTCACCATGTCTCTTTATGCGATTTCCGCGATTGTGGTCTGTTCTGTCTTGCCGCACCTTTATGAAA
GCTGGGCCGTGCGTTATCGGTTATTTGGTCTGCTTTGGGTGTCTTGGGTGCCGTTGTAGCAACCTTGATGCGTGG
ATTGTGCAATGACGTCTATTTCCAGATCGGTTTGTGACGACCGTTGGTTTACCCTTAAAAACGCTATTTTGTATTGTC
GAATTTGCAAAAGCCTTTTTCGATAATGGCGTGCCACTTTTGAATCGGTGGTTCAAGCAGGCGGTGAGCGGTTACGGC
CTATTTTGTGACCTCTATTGCTTTTGTGTTGGGGTTATTCCATTGAGCATCGCAACAGGGGCTTCTTCGGCAGCAGC
TATCGCTATCGGAACGGCCGTTGTCGGCGGGATGGTACGGCTACCTTGTGACGATTTTCTTTGTGCCTCTTTCTTT
GTGGTGGTTTTGAAGCTGTTTCCGGTGAAACCGAACAAGCTGAATGCGGAGGAAGCAGCCTGA

B. SEQ ID NO:12

MARYFIDRPVFAWVIGLIIMLLGALAIKMPIAQYPNVAPPQIEISVSYPGASAETINNTVVRPILQQMHGIDNLEYIS
ASSFASGQMTIDLTFAGQTDADIAQVQVQNKQLQAQPRLPDQVNVQGITVNRSAKSFMMIMSFISTDGSMSYQDINDYV
ASNIADPLSRVSGVDYTLFGFEYAMRVWLDPAKLYKYNLTADVQSAISTQNIQLSSGELGGLPAVQGI RL DATI IGP
TRLTSPEEFKNI LVKALPDGAQIKLGDIAKVELGAQSYNFDVRYNNQPASGIAIKLAPGANQLQTEKLI RQRLADLEPF
FPHGLKVEYPVDTKPFVTAS IHEVIETLVEAIALVFLVMLIFLQNFRA TL IPTIAVPVLLGTFGVLSVLGFSINTLTM
LAMVLAVGLLVDDAIVVVENVERLMRDEKLPKKAARSMDEISGALIGIVLVL SAVFLPMAAFSGSTGVIYRQFSITI
VVAMGLSVLVAMIMTPALCATMLKPIDHDQADKKPGIFGRLANGFNRAFDRLNNGYLGGVSWLLGRSVKGGIAFLIIVF
AVGYLFTRLPTGFLPDEDQGEFIGQVTLPPGATQEQTSEAVRKVNDYLLSAEKDSVIVSMTVSGFNFGGQGNAGSFFV
RLKPWDQRPKASQSASALAMRTMMHFWGDPSSMTFAFNMPAVRDLGNATGFDLELEDRGHIGHAKFLEARNMLLALASK
DPRLSGVRPNGMEDAPQYHLTVDYGKAVMMGLTPNDVNVALQGSLSIYVNQFMRDRVKQVYLMGAPPEARMLPSDFSK
WYLRNNVGTMPVPSAFMTGTWQTPQKVENYNGYNSFEIMGAPAPGHSSGEAIQAMTEIVHKLPAVGHEWTGLSFEEQ
AAGSSTMSLYAISAI VVLFCLAALYESWAVPLSVILVPLGLVAVVATLMRGLSNDVYFQIGLLTTVGLTVKNAI L I V
EFAKAFFDNGVPLQSVVQAGRERLRPILMTSIAFVLGVIPLSIATGASSAARIAIGTAVVGGMVTATLLTIFVPLFF
VVVLKLFVRKPNKLNAAA

Figure 7

A. SEQ ID NO:13

ATGACTTTATTTTCGGCTTCTTCGGCTCTGATTAAGCGGAGTAAAAAGGATGGCGTTATCC
TGTAACGCTATTCTTATCGACTAATATTCTGTTGGCTGGATGCACGATGGCACCGAAATATC
ATCGTCCAGCAGCGTCTGTGGCACCGCAATGGCCGAAATCAGCGGCATTGCCTGCCGCTGAT
AACACTTCAATGAAGCCCCATCCTATGGCAGCCGATTTGGGGTGGCAGGATTTTTTCAAAGA
TGCGCGCCTAAAAGCCCTGATTACAATTGCGATCCGCGAAAACCGCGATTTGCGGTCAGCTA
TTCAGGCAATCGGTGAGGCGCAAGCCAGATATCGAGTCAACGCGCGTCTTTATTGCCGCA
ATCGGTGGCACTGGCGAAGTGATGTATCAGCAGCCTTCGGGTAAATCCGGTTTGGTTTTGC
CCCAGGTGTCGGTGAAGATATTCCGCGTTTCCATTATTATTTCGATGGGTATCGGTTTTTCTT
CTTATGAAATTGATATTTTTGGCCGCATCCGCAGTTTAAGCAAGGAGGCGGCTGAAAGAGCC
TTGATGCAGGAAGAGACTGCCAGAGGCACCTTGATCACGCTGATTTTCGAGGTGGCAAATAG
CTATATTGCTTGGTTGGCAGATCGAGAACTTTGAATCTTGCCGAAGAAAGCTATCAGGCTG
CCAAGCGGAATTTGGATTTGACGCAGGCTTTGCTTGACCATGGTGAAGCGAGCCTTTTGACG
GTCAATCAAGCCGAAACCTTGTTCCAGCAAAAAGCAGATTTGCGGGAGCAGGCAAAGCGTCA
GATGGCATGGGAAGAAAATAATCTTGTCTTGCTGATCGGGCAGCCTTTGCCCGATAATTTGC
CGCCGCTTTGCCCTTTGGTGAGCAAAAATCATCGAAGATTTATCGCCCGGTTTGCCTTCC
GATCTTTTGGAAAACCGGCCTGATATTCGAGCCGCGGAACATGATTTAAAGGCCGCTAATGC
GGATATTGGGGCAGCAAGAGCGGCTTTTTTCCCAAGGTTGTCTTTGACCTCTTCGGTTGGTA
ACTCAAGCCTTAAGCCTTCCAGATTTTCACTACAGCGGCAATACATGGGGATTCCAACCG
GAATTGACCGTGCTATTTTTAACTGGGGGCAAAATCGCGCAATTTGAGAATTTCCAAGGC
CGAGCGCGATATGAAGATCACGGCCTATCAAAAAGCAATCCAAAGTGCTTTTCGTGATGTGT
CGAATGCTTTAGTCGGACGCGATACTTATCGTCTGAGGAAGTCGCTTGACTCAAGCGGCG
GCGAAGGCTGAAAATAACTGGAATTTAGCGCGTTTGCCTCAGACTCAAGGCAGTGATTCGCG
CATCACTATGCTTAATTACGAGCAGACTTATTACCAAGCGGAATATCAGGCGATACAGAACA
GGGTTGCGCGTTATCAAAATTTGGTGACGCTCTATTCCGCTTTGGGCGGTGGGGTGAAGAA
AAAGCGGTATCTTTGGATAAACTGATAAAGCCGCCCATTTCTGCCATTGA

B. SEQ ID NO:14

MTLFSASSALIKRSKKGWRYPVTLFLSTNILLAGCTMAPKYHRPAASVAPQWPKSAALPAAD
NTSMKPHPMAADLWQDFFKDARLKALITIAIRENRDLRSIQAIQGEAQARYRVQRASLLPA
IGGTGEVMYQQPSGKSGLSFAPGVGEDIPRFHYYSMGIGFSSYEIDIFGRIRLSKEAAERA
LMQEETARGTLITLISQVANSYIAWLADRETLNLAESYQAAKRNLDLTQALLDHGEASLLT
VNQAETLFQOKADLREQAKROMAWEENLVLLIGQPLPDNLPPPLPFGEQNI IEDLSPGLPS
DLLENRPDIRAAEHDLKAANADIGAARAAFFPRLSLTSSVGNSSLKPSQIFTTAANTWGFQP
ELTVPIFNWQNRANLRISKAERDMKITAYQKAIQSAFRDVSNALVGRDITYRREEVALTQAA
AKAENNWNLARLRQTQGSDAITMLNQEYQAEYQAIQNRVARYQNLVTLYSALGGGVKE
KAVSLDKTDKAAHSAH

Figure 8

A. SEQ ID NO:15

ATGACACCCGATCAATCCGATAAAAAGCGCCTCAAAACGCCATGTAGGGCGGCCTCCACAGCT
TGATGAAAAAAAAACGCTGTGCTCTTATCTTAAAAGCCGCTGCAACGGTGCTGCAAACGCATG
GCTATGATGGTTCAGTATGGATCGGGTTGCCAGTCAGGCAGGCATGTCAAAAAGACGGTG
TATCAAATGTTCCCGTCAAAAAGATATTATTACCAAATTAATCGAAGATCGGCTTTTCTC
GATTGAATGGCCAGAAGAAAAAATCTGCGAAGACCCCGAAGAACATCTCTACTCTCTATTGA
TCGCCATTGCTCAAACCTATTCTAAGGCCGGATCGGGTCTGCCTGCTTCGCATTTTAACCGTC
GAACATAAATCAGAAGAAATGCGGCATATTTTATAGTGATATTTTACAAGGACATACTGAAGA
CAATTTGACGCGCTGGTTCTCCGAACAACAAGACAAAGGTCGCTACCATATATCCGACCCCA
TAAAATATGCGGATATCATTTTAAATATGACCGTAGGCAGCCTGTTGCTCGATCGACTTTTC
GGTTTAGAAAAACGCCCTGTTGAAGACAATTTTCGAGATGCCATTTCAATTTTTTTACGGGG
TATCCGTATCAATCCTGAAAATGAATAA

B. SEQ ID NO:16

MTPDQSDKSASKRHVGRPPQLDEKKRCALILKAAATVLQTHGYDGS SMDRVASQAGMSKKT
YQMFPSKKILFTKLLEDRLFSEIEWPEEKICEDPEEHLYSLLIAIAQTILRPDRVCLLRILTV
EHKSEEMRHI FSDILQGHTE DNLTRWFSEQQDKGRYHISDP IKYADIIFNMTVGSLLLDRLF
GLEKRPVEDNFRDAISIFLRGIRINPENE

Figure 9



Figure 10A

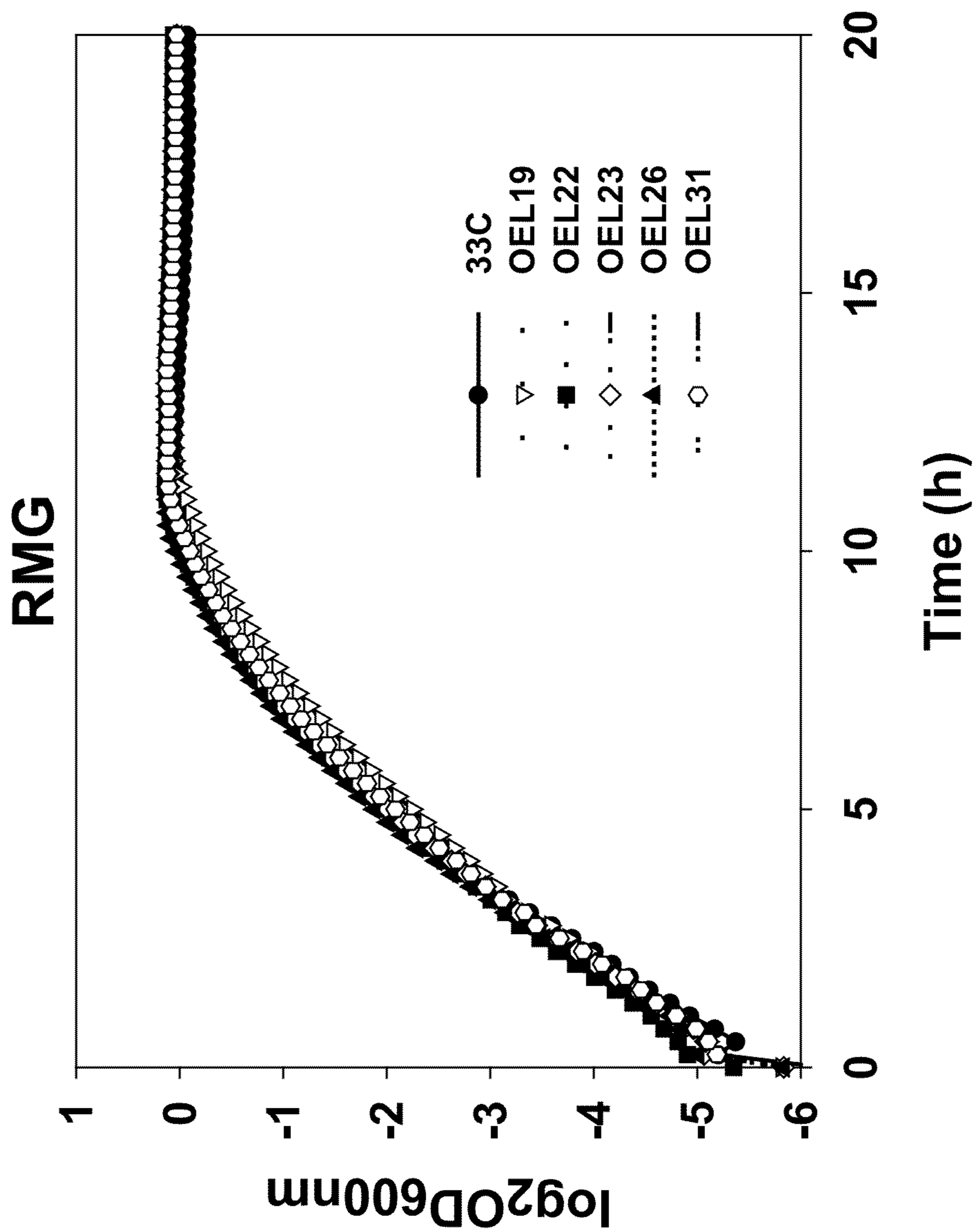


Figure 10B

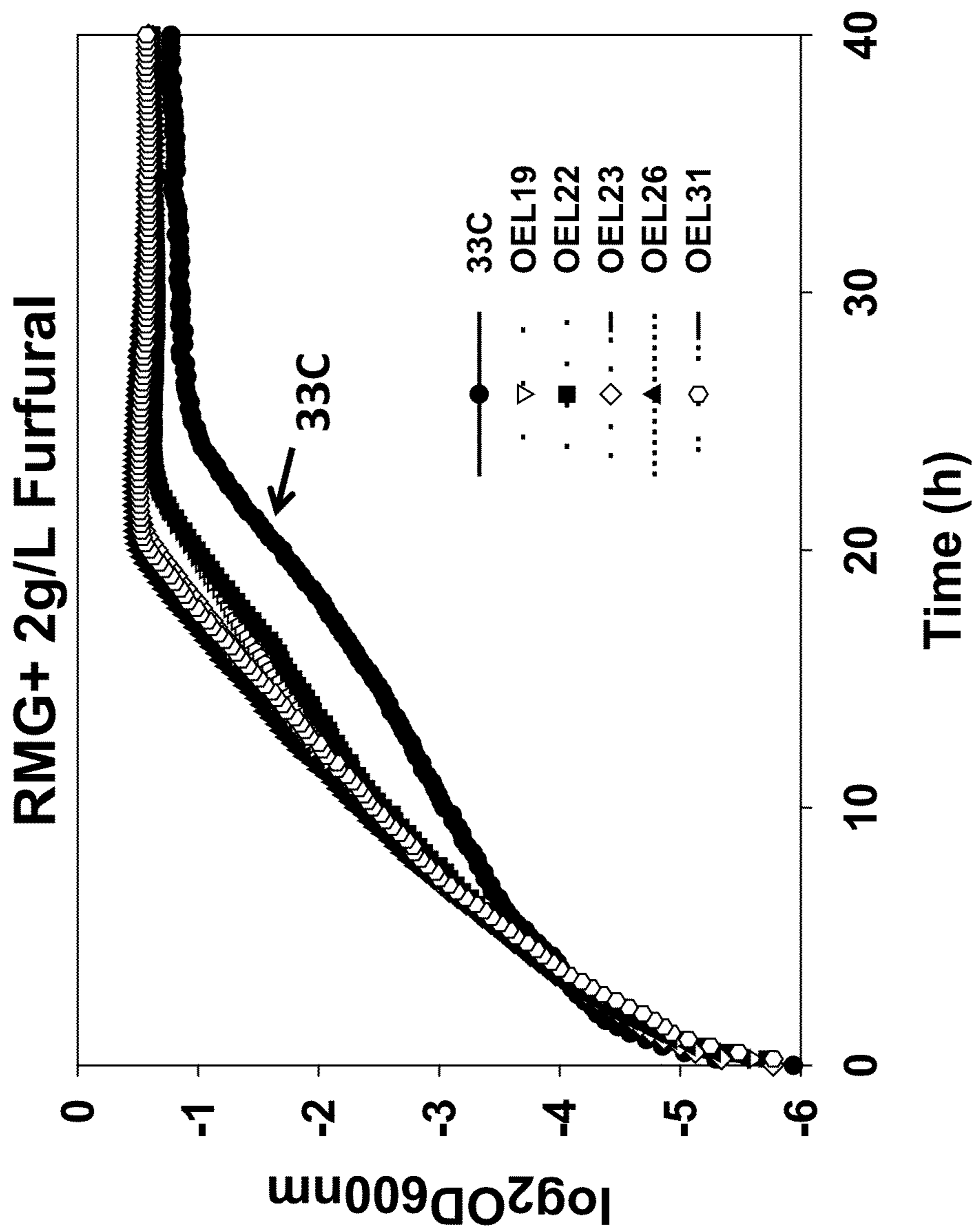


Figure 10C

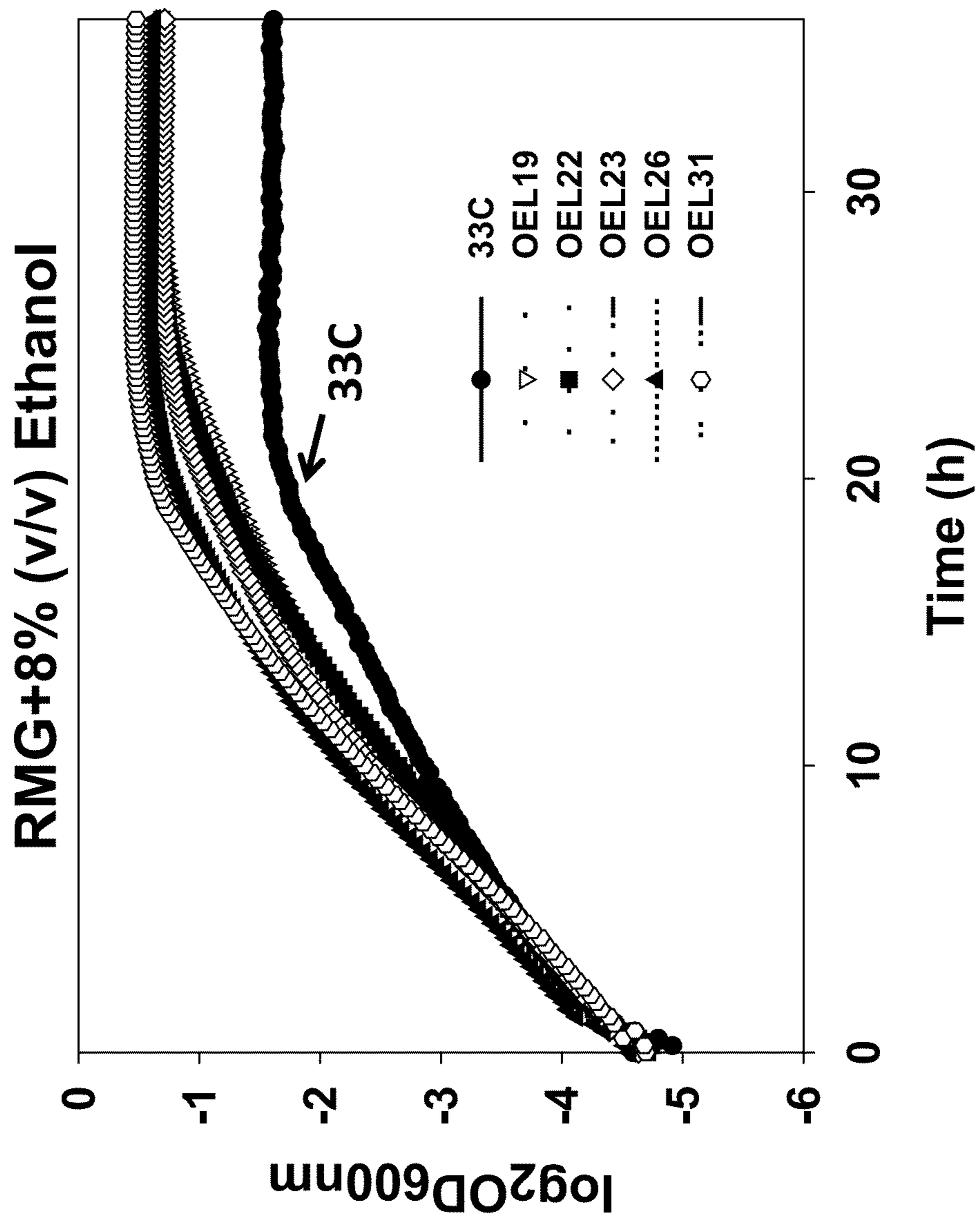


Figure 11

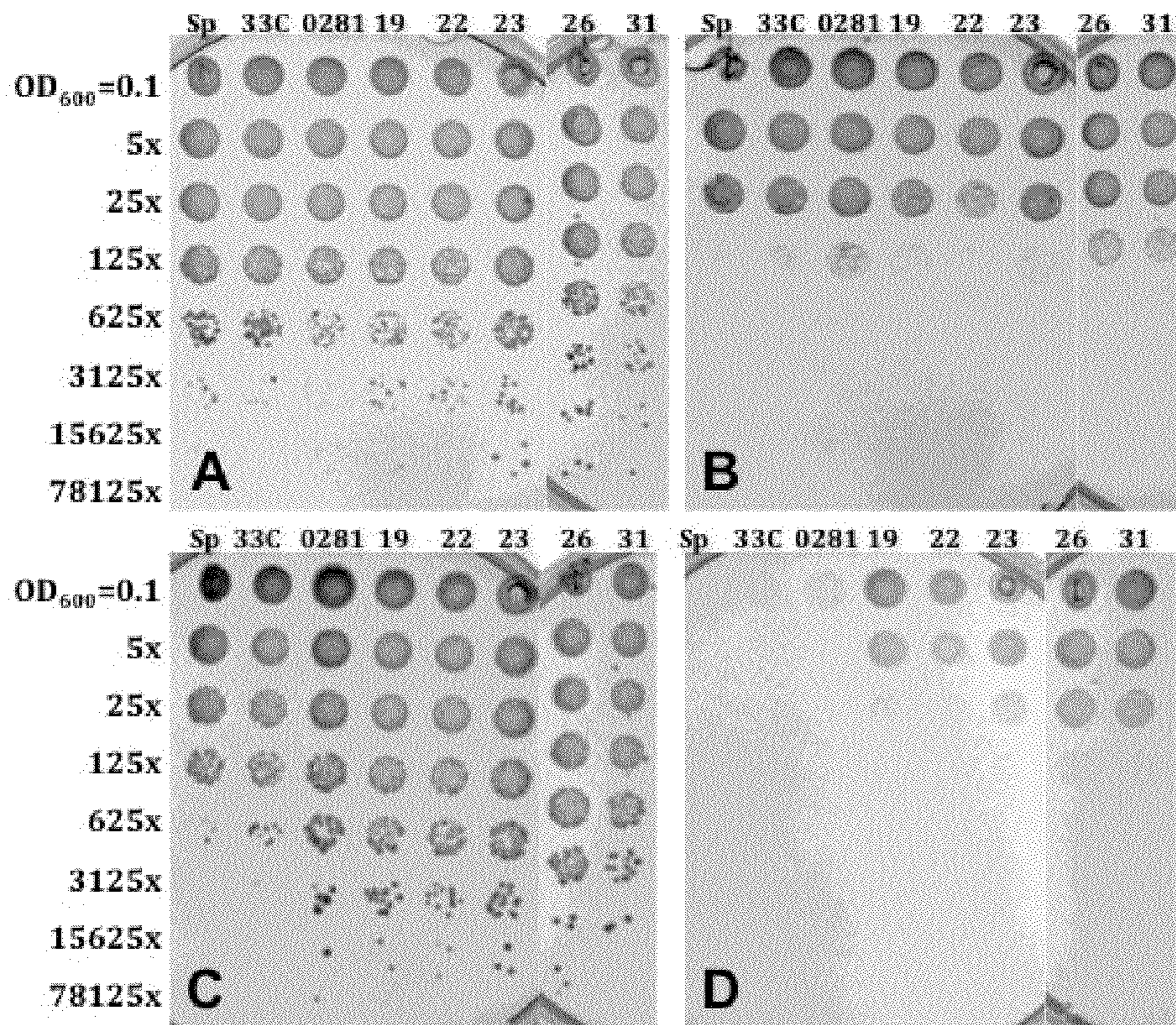


Figure 12

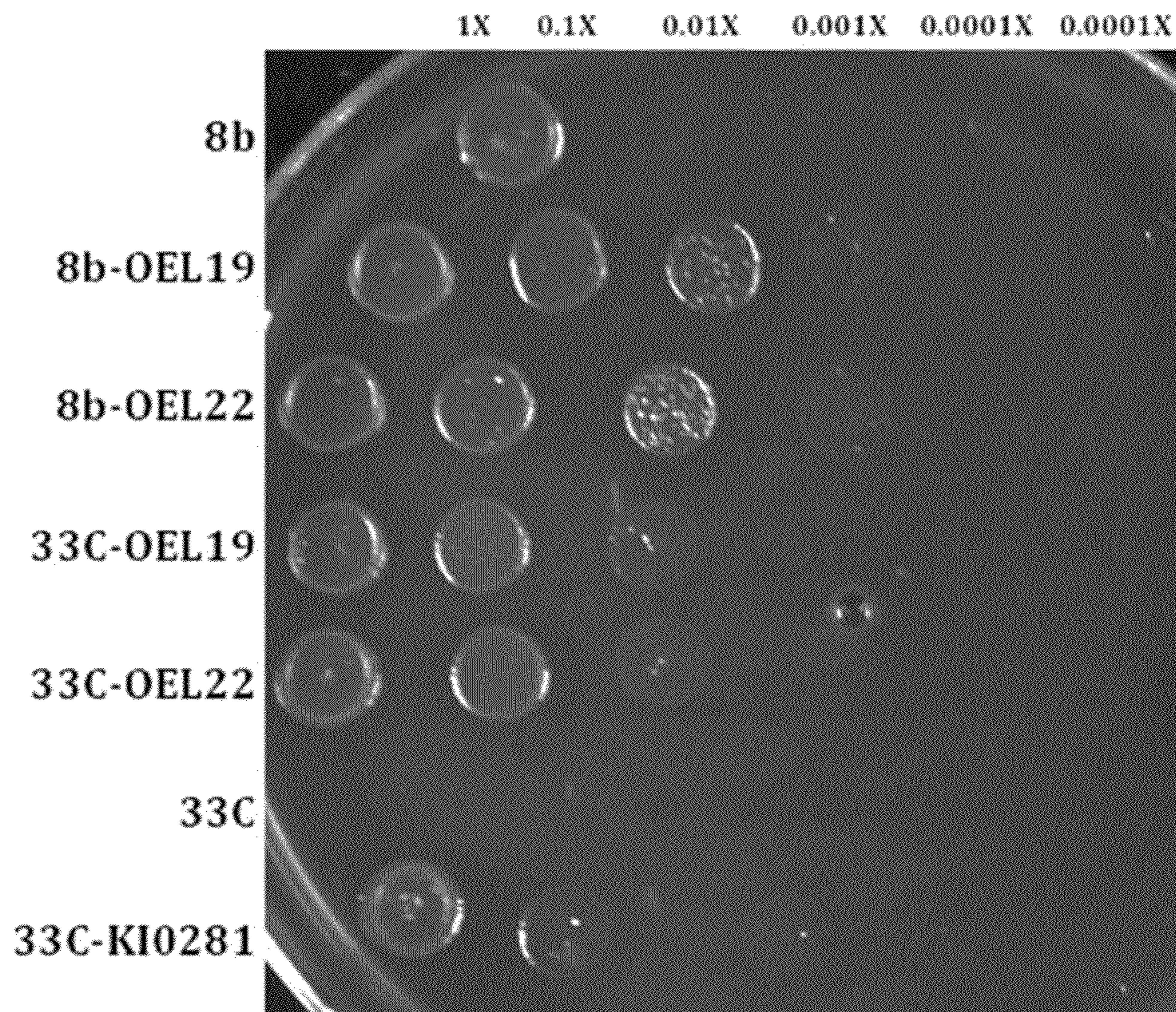
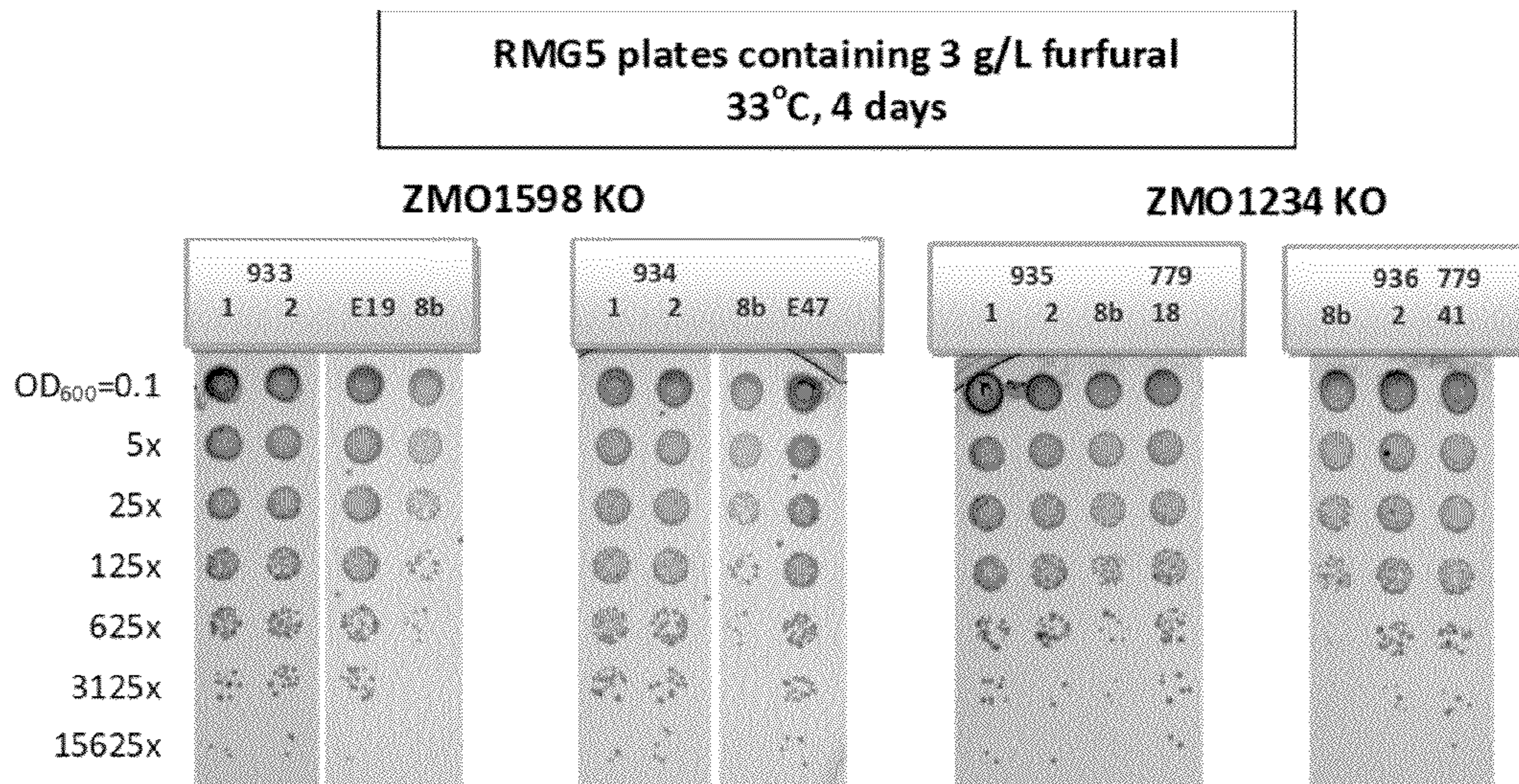


Figure 13



**BIOCATALYSTS WITH ENHANCED
INHIBITOR TOLERANCE**CROSS-REFERENCE TO RELATED
APPLICATIONS

This application claims priority to U.S. Provisional Application No. 61/817,053, filed Apr. 29, 2013, the contents of which are incorporated by reference in their entirety.

CONTRACTUAL ORIGIN

The United States Government has rights in this invention under Contract No. DE-AC36-08GO28308 between the United States Department of Energy and Alliance for Sustainable Energy, LLC, the Manager and Operator of the National Renewable Energy Laboratory.

REFERENCE TO SEQUENCE LISTING

This application contains a Sequence Listing submitted as an electronic text file entitled "13-22_ST25.txt," having a size in bytes of 84 kb and created on Aug. 4, 2014. Pursuant to 37 CFR §1.52(e)(5), the information contained in the above electronic file is hereby incorporated by reference in its entirety.

BACKGROUND

Biofuels derived from lignocellulosic biomass represent an alternative to petroleum based transportation fuels that take advantage of an abundant and renewable resource while not utilizing food crops as feedstocks. Cellulose and hemicellulose found in biomass, however, must first be converted to fermentable sugars, which are in turn converted to biofuels such as ethanol by fermentative organisms.

Numerous methods have been developed to convert biomass cellulose and hemicellulose fractions to sugars, including treatment with enzymes or chemicals. Pretreatment of biomass feedstocks with dilute acid is a technique frequently used to hydrolyze hemicellulose and improve the susceptibility of cellulose to enzymatic degradation, but this process can create compounds that inhibit the subsequent fermentation of sugars to biofuels. Methods to detoxify the pretreated feedstocks are often not economical or reduce the amount of sugars available for fermentation.

The existence of multiple inhibitors within feedstocks such as corn stover treated with dilute sulfuric acid restrains the growth of biocatalyst organisms leading to low ethanol yield and/or prolonged fermentation processes. Development of robust biocatalysts with enhanced tolerance to feedstock inhibitor compounds is needed for the economical production of biofuels.

The foregoing examples of the related art and limitations related therewith are intended to be illustrative and not exclusive. Other limitations of the related art will become apparent to those of skill in the art upon a reading of the specification and a study of the drawings.

SUMMARY

The following embodiments and aspects thereof are described and illustrated in conjunction with systems, tools and methods that are meant to be exemplary and illustrative, not limiting in scope. In various embodiments, one or more of the above-described problems have been reduced or eliminated, while other embodiments are directed to other improvements.

Exemplary embodiments provide microorganisms comprising a genetic modification that increases the growth rate or biofuel production rate of the modified microorganism in the presence of a feedstock inhibitor compound relative to the growth rate or biofuel production rate of the unmodified microorganism.

In some embodiments, the genetic modification increases the expression or activity of a histidine kinase such as ZMO1162 relative to the expression or activity level in the unmodified microorganism. In others, the genetic modification decreases the expression or activity of (or abolishes the function of) a functional sigma-54 modulation protein such as ZMO0038 relative to the expression or activity level in the unmodified microorganism.

In certain embodiments, the microorganism is a bacterium, is a strain from the genus *Zymomonas*, or is a strain of *Zymomonas mobilis*.

In some embodiments, the feedstock is corn stover, or corn stover pretreated with a dilute acid.

In various embodiments, the feedstock inhibitor compound comprises furfural and the biofuel is ethanol.

Additional embodiments provide methods for producing a biofuel by culturing a microorganism as disclosed herein with a feedstock under conditions whereby the microorganism ferments the feedstock into a biofuel and isolating the biofuel from the culture.

In certain embodiments, the feedstock is lignocellulosic biomass, lignocellulosic biomass that has been pretreated with acid or enzymes to produce fermentable sugars, or acid pretreated corn stover hydrolysate.

In some embodiments, the feedstock comprises fermentable sugars and at least one inhibitor compound, which may be furfural.

In certain embodiments, the biofuel is ethanol.

In addition to the exemplary aspects and embodiments described above, further aspects and embodiments will become apparent by reference to the drawings and by study of the following descriptions.

BRIEF DESCRIPTION OF THE DRAWINGS

Exemplary embodiments are illustrated in referenced figures of the drawings. It is intended that the embodiments and figures disclosed herein are to be considered illustrative rather than limiting.

FIG. 1 shows the nucleic acid (A) and amino acid (B) sequences for ZMO1162.

FIG. 2 shows the nucleic acid (A) and amino acid (B) sequences for ZMO0038.

FIG. 3 shows the nucleic acid (A) and amino acid (B) sequences for ZMO1598.

FIG. 4 shows the nucleic acid (A) and amino acid (B) sequences for ZMO1234.

FIG. 5 shows the nucleic acid (A) and amino acid (B) sequences for ZMO0282.

FIG. 6 shows the nucleic acid (A) and amino acid (B) sequences for ZMO0283.

FIG. 7 shows the nucleic acid (A) and amino acid (B) sequences for ZMO0285.

FIG. 8 shows the nucleic acid (A) and amino acid (B) sequences for ZMO0281.

FIG. 9 shows the results of a hydrolysate plate assay for *Zymomonas* strains exhibiting enhanced tolerance to hydrolysate (OEL19, OEL22, OEL23, OEL26, OEL31), along with control strains 33C(pJL12), 33C and 8b.

FIG. 10 shows growth assay results for five strains (OEL19, 22, 23, 26, and 31) with enhanced hydrolysate tol-

erance and the parental strain 33C in media only (A), media supplemented with 2 g/L furfural (B), and media supplemented with of 8% (v/v) ethanol.

FIG. 11 shows the results of furfural sensitivity assays for *Zymomonas* strains OEL19 (19), OEL22 (22), OEL23 (23), OEL26 (26), OEL31 (31), and a strain that overexpresses ZMO0281 (0281), each with enhanced hydrolysate tolerance compared to their parental strain 33C as well as a control strain 33C-Sp (Sp). Shown are plates with 0 g/L furfural (A), 2 g/L furfural (B), 3 g/L furfural (C), and 4 g/L furfural (D).

FIG. 12 shows the results of a 40% hydrolysate plate assay for unmodified *Zymomonas* strains (8b and 33C) and strains with modifications to ZMO0038 (8b-OEL19 and 33C-OEL19) or ZMO1162 (8b-OEL22 and 33C-OEL22).

FIG. 13 shows the results of furfural sensitivity assays for *Zymomonas* strains with knockouts of ZMO1598 (#933 and #934) and ZMO1234 (#935 and #936) compared with control isolates from the knockout library (E19, E47, 779-18, and 779-41) on RMG agar plates containing 3 g/L furfural.

DETAILED DESCRIPTION

Disclosed herein are biocatalysts for the production of biofuels. The biocatalysts are microorganisms that contain genetic modifications conferring tolerance to growth or fermentation inhibitors found in many cellulosic feedstocks, including those feedstocks that have been pretreated with chemicals such as dilute acids. Methods of converting cellulose-containing materials to fuels and chemicals, as well as methods of fermenting sugars to fuels and chemicals, using these biocatalysts are also disclosed.

Genetic loci have been identified that confer tolerance to inhibitor compounds found in feedstocks used for fermentation into biofuels. Modification of these loci in a microorganism may result in a biocatalyst organism able to grow at an increased rate or grow to a higher concentration in culture relative to the unmodified organism in the presence of inhibitor compounds. Modification of these loci in a microorganism may also result in a biocatalyst organism able to produce a biofuel at a higher rate or to a higher concentration in culture relative to the unmodified organism in the presence of inhibitor compounds. An organism with enhanced tolerance to an inhibitor compound exhibits enhanced growth or biofuel production in the presence of the inhibitor compound in comparison to a less tolerant organism.

As used herein, the term “inhibitor compound” or “inhibitor” refers to a compound that interferes with the overall sugar fermentative capabilities of an organism. Many inhibitor compounds exist that interfere with the growth or fermentation properties of biocatalyst organisms, including those naturally found in biomass feedstocks, generated by pretreatment of the feedstock with chemicals such as dilute acids or bases, or generated via fermentation of a feedstock-derived sugars by an organism. Examples include acetate or furfural compounds commonly found in acid pretreated corn stover. Additional inhibitor compounds include furfuraldehydes such as hydroxymethylfurfural, weak acids (e.g., acetic acid, levulinic acid or formic acid), syringic acid, p-hydroxybenzoic acid, vanillin, terpenoids, phenolics and aromatics (e.g., benzoate). Inhibitor compounds also include metabolic byproducts (e.g., lactate or acetate) and an increased concentration of the fermentation product being generated (e.g., ethanol).

A genetic modification conferring tolerance may include any modification that results in a gain or loss of function at a particular genetic locus. Such modifications may be within sequences that encode gene products or in noncoding regions

that influence gene expression. Modifications may also include the insertion of sequences known to increase or decrease gene expression (e.g., promoters, enhancers and the like). For example, the genetic modification may be an insertion into a gene coding sequence that ablates or attenuates the expression of the polypeptide encoded by the gene. In other embodiments, the genetic modification may be the insertion of a promoter into a noncoding region of a host genome that results in enhanced expression of a gene product. In still other embodiments, the genetic modification may result in a truncated or disrupted gene encoding an altered polypeptide with an augmented or reduced activity relative to the wild type polypeptide.

In certain embodiments, the genetic modification may be a modification of a gene encoding a histidine kinase, such as a PhoR protein or homologs thereof. One exemplary histidine kinase gene from *Z. mobilis* is designated ZMO1162. The nucleotide sequence for ZMO1162 (SEQ ID NO:1) and the amino acid sequence encoded by ZMO1162 (SEQ ID NO:2) are provided in FIG. 1. However, additional histidine kinases from other bacteria or microorganisms may also be modified. Examples include the PhoR histidine kinase from *Escherichia coli* or *Bacillus subtilis*, as well as the SLN1 gene product from yeast such as *S. cerevisiae*.

The genetic modification may be the overexpression of a histidine kinase gene or a modification of the histidine kinase gene that results in a histidine kinase with increased enzymatic activity. The modification may result in increased expression or activity of an endogenous histidine kinase or the expression of an exogenous histidine kinase (e.g., via introducing an expression vector including a nucleic acid encoding a histidine kinase) in a microorganism to increase overall expression or activity levels. In certain embodiments, the modification may be the insertion of a promoter into the genome of a microorganism near the gene encoding a histidine kinase to increase expression of the histidine kinase. For example, the promoter Pgap may be inserted into the genome of a *Zymomonas* strain to increase expression of ZMO1162.

In other embodiments, the genetic modification may be a modification of a gene encoding a sigma-54 modulation protein or a homolog thereof. One exemplary sigma-54 modulation protein from *Z. mobilis* is designated ZMO0038. The nucleotide sequence for ZMO0038 (SEQ ID NO:3) and the amino acid sequence encoded by ZMO0038 (SEQ ID NO:4) are provided in FIG. 2. However, additional sigma-54 modulation proteins from other bacteria or microorganisms may also be modified. Examples include the Hst23 protein (UniProtKB Entry P28368) from *Bacillus subtilis* and the Ccel 0370 protein from *Clostridium cellulolyticum*. The N-terminal portion of ZMO0038 contains a conserved domain of Ribosome-associated Inhibitor A (RaiA, also known as Protein Y [PY], YfiA, and SpotY), which is a stress-response protein that binds the ribosomal subunit interface and arrests translation by interfering with aminoacyl-tRNA binding to the ribosomal A site. Suitable sigma-54 modulation proteins also include proteins containing a RaiA domain.

The genetic modification may be an alteration of a gene resulting in the deletion of a functional sigma-54 modulation protein by ablation of the gene or other alteration leading to expression of a nonfunctional sigma-54 modulation protein. The modification may result in decreased expression or activity of an endogenous sigma-54 modulation protein. In certain embodiments, the modification may be the insertion of a nucleotide sequence into the genome of a microorganism within the gene encoding a sigma-54 modulation protein to decrease or ablate the expression of the functional sigma-54 modulation protein. For example, a nucleotide sequence may

be inserted into the genome of a *Zymomonas* strain to reduce or ablate expression of ZMO0038.

In certain embodiments, the genetic modification may be a modification of a gene encoding a 1-deoxy-D-xylulose-5-phosphate synthase (Dxs) or a homolog thereof. Two exemplary Dxs enzymes from *Z. mobilis* are designated ZMO1598 and ZMO1234. The nucleotide sequence for ZMO1598 (SEQ ID NO:5) and the amino acid sequence encoded by ZMO1598 (SEQ ID NO:6) are provided in FIG. 3. The nucleotide sequence for ZMO1234 (SEQ ID NO:7) and the amino acid sequence encoded by ZMO1234 (SEQ ID NO:8) are provided in FIG. 4. However, additional Dxs enzymes from other bacteria or microorganisms may also be modified.

The genetic modification may be an alteration of a gene resulting in the deletion of a functional Dxs enzyme by ablation of the gene or other alteration leading to expression of a nonfunctional Dxs enzyme. The modification may result in decreased expression or activity of an endogenous Dxs enzyme. In certain embodiments, the modification may be the insertion of a nucleotide sequence into the genome of a microorganism within the gene encoding a Dxs enzyme to decrease or ablate the expression of the functional Dxs enzyme. For example, a nucleotide sequence may be inserted into the genome of a *Zymomonas* strain to reduce or ablate expression of ZMO1598 or ZMO1234.

In some embodiments, the genetic modification may be a modification of a gene encoding a component of a membrane-bound efflux transport system. For example, the genes from *Z. mobilis* designated ZMO0282, ZMO0283, and ZMO0285 are located on the same operon and exhibit similarity to genes from *E. coli* that function as components of efflux transporter complexes. The nucleotide sequence for ZMO0282 (SEQ ID NO:9) and the amino acid sequence encoded by ZMO0282 (SEQ ID NO:10) are provided in FIG. 5. The nucleotide sequence for ZMO0283 (SEQ ID NO:11) and the amino acid sequence encoded by ZMO0283 (SEQ ID NO:12) are provided in FIG. 6. The nucleotide sequence for ZMO0285 (SEQ ID NO:13) and the amino acid sequence encoded by ZMO0285 (SEQ ID NO:14) are provided in FIG. 7. However, additional membrane-bound efflux transport systems from other bacteria or microorganisms may also be modified.

The genetic modification may be an alteration of a gene resulting in the deletion of a functional efflux transport system protein by ablation of the gene or other alteration leading to expression of a nonfunctional protein. The modification may result in decreased expression or activity of an endogenous efflux transport system protein. In certain embodiments, the modification may be the insertion of a nucleotide sequence into the genome of a microorganism within the gene encoding an efflux transport system protein to decrease or ablate the expression of the functional protein. For example, a nucleotide sequence may be inserted into the genome of a *Zymomonas* strain to reduce or ablate expression of ZMO0282, ZMO0283, or ZMO0285. In certain embodiments, the modification may result in the reduced expression of at least one gene within the operon containing ZMO0282, ZMO0283, and ZMO0285.

The genetic modification may also be to a TetR family repressor, such as ZMO0281. The nucleotide sequence for ZMO0281 (SEQ ID NO:15) and the amino acid sequence encoded by ZMO0281 (SEQ ID NO:16) are provided in FIG. 8. The genetic modification may be the overexpression of a repressor gene that may result in lower expression or activity of an efflux transport system protein. The modification may result in increased expression or activity of the repressor (e.g., via introducing an expression vector including a nucleic acid encoding a repressor) in a microorganism to increase overall

expression or activity levels. In certain embodiments, the modification may be the insertion of a promoter into the genome of a microorganism near the gene encoding a TetR family repressor to increase its expression. For example, the promoter Pgap may be inserted into the genome of a *Zymomonas* strain to increase expression of ZMO0281.

Without wishing to be bound to any particular theory, the ZMO0281 gene product may act to repress the expression of ZMO0282, ZMO0283, and ZMO0285. ZMO0281 has similarity to AcrR of *E. coli*, while the genes ZMO0282 and ZMO0283 have structural similarities to AcrA and AcrB. In *E. coli*, AcrAB is part of the RND family of efflux transporters and is implicated in tolerance to organic solvents. Its deletion in *E. coli* results in a hypersensitivity to organic solvents. It is repressed by the AcrR regulator, a DNA binding protein which binds to the operator element for both *acrAB* and *acrR*. AcrAB complexes with TolC, an outer membrane protein, which has similarities in function to the ZMO0285 gene product of *Zymomonas*. Unlike *E. coli*, disruption of ZMO0282 and ZMO0283 and overexpression of ZMO0281 do not lead to increased sensitivity to furfural. Instead, the opposite effect is observed in *Z. mobilis*, which indicates that the efflux pump complex involving ZMO0282 and ZMO0283 may play a negative role in furfural resistance.

In exemplary embodiments, the microorganism may be a bacterium such as one from the genus *Zymomonas*, from the species *Zymomonas mobilis*, or a strain of *Z. mobilis* such as *Z. mobilis* strains 33C, 8b, 39676, CP4, or ZM4. *Z. mobilis* has proven to be an extremely valuable organism in the conversion of biomass-derived sugars to ethanol. In addition to its fermentative abilities, *Z. mobilis* cells expressing nucleic acids encoding cellulases and other enzymes may also play a significant role in the degradation of lignocellulosic biomass. Given the proven adeptness of *Z. mobilis* in industrial-scale fermentation, a demonstrated ability to express and secrete high levels of active cellulases, *Z. mobilis* may be particularly suitable as organism for both the degradation of biomass to sugars and the subsequent fermentation of sugars to biofuels. Additional suitable microorganisms include bacteria such as *E. coli* or strains from the genera *Clostridium* (e.g., *C. cellulolyticum* or *C. thermocellum*) or *Bacillus* (e.g., *B. subtilis*) and yeasts such as those from the genus *Saccharomyces* (e.g., *S. cerevisiae* or *S. pombe*) or *Pichia* (e.g., *P. pastoris*).

Suitable *Zymomonas* cells include cells previously transformed with expression vectors containing genes useful in the degradation of biomass or the fermentation of sugars into ethanol and other industrial chemicals. Examples include *Zymomonas* cells capable of utilizing pentose sugars such as xylose or arabinose as a carbon source, as described, for example in U.S. Pat. Nos. 5,514,583; 5,843,760; 6,566,107; and 7,223,575.

Although the production of ethanol from acid pretreated corn stover hydrolysate is exemplified herein, a variety of feedstocks and biofuels are contemplated. Exemplary biofuels include ethanol, propanol, butanol and other alcohols, as well as advanced hydrocarbon biofuel candidates and intermediates. Feedstocks include any capable of supplying fermentable sugars, including sugars generated by subjecting cellulosic materials to heat, enzymes, or chemicals. Typical biofuel production processes involve pretreating biomass to convert cellulose and hemicellulose to oligosaccharides, which are then enzymatically hydrolyzed to simple sugars, which are in turn fermented by microorganisms to biofuels. Suitable feedstocks include any biomass or cellulose-containing materials such as acid pretreated corn stover hydrolysate.

“Nucleic acid” or “polynucleotide” as used herein refers to purine- and pyrimidine-containing polymers of any length, either polyribonucleotides or polydeoxyribonucleotide or mixed polyribo-polydeoxyribonucleotides. This includes single- and double-stranded molecules (i.e., DNA-DNA, DNA-RNA and RNA-RNA hybrids) as well as “protein nucleic acids” (PNA) formed by conjugating bases to an amino acid backbone. This also includes nucleic acids containing modified bases.

Nucleic acids referred to herein as “isolated” are nucleic acids that have been removed from their natural milieu or separated away from the nucleic acids of the genomic DNA or cellular RNA of their source of origin (e.g., as it exists in cells or in a mixture of nucleic acids such as a library), and may have undergone further processing. Isolated nucleic acids include nucleic acids obtained by methods described herein, similar methods or other suitable methods, including essentially pure nucleic acids, nucleic acids produced by chemical synthesis, by combinations of biological and chemical methods, and recombinant nucleic acids that are isolated.

Nucleic acids referred to herein as “recombinant” are nucleic acids which have been produced by recombinant DNA methodology, including those nucleic acids that are generated by procedures that rely upon a method of artificial replication, such as the polymerase chain reaction (PCR) and/or cloning into a vector using restriction enzymes. Recombinant nucleic acids also include those that result from recombination events that occur through the natural mechanisms of cells, but are selected for after the introduction to the cells of nucleic acids designed to allow or make probable a desired recombination event. Portions of isolated nucleic acids that code for polypeptides having a certain function can be identified and isolated by, for example, the method disclosed in U.S. Pat. No. 4,952,501.

An isolated nucleic acid molecule can be isolated from its natural source or produced using recombinant DNA technology (e.g., polymerase chain reaction (PCR) amplification, cloning) or chemical synthesis. Isolated nucleic acid molecules can include, for example, genes, natural allelic variants of genes, coding regions or portions thereof, and coding and/or regulatory regions modified by nucleotide insertions, deletions, substitutions, and/or inversions in a manner such that the modifications do not substantially interfere with the nucleic acid molecule’s ability to encode a polypeptide or to form stable hybrids under stringent conditions with natural gene isolates. An isolated nucleic acid molecule can include degeneracies. As used herein, nucleotide degeneracy refers to the phenomenon that one amino acid can be encoded by different nucleotide codons. Thus, the nucleic acid sequence of a nucleic acid molecule that encodes a protein or polypeptide can vary due to degeneracies.

A nucleic acid molecule is not required to encode a protein having protein activity. A nucleic acid molecule can encode a truncated, mutated or inactive protein, for example. In addition, nucleic acid molecules may also be useful as probes and primers for the identification, isolation and/or purification of other nucleic acid molecules, independent of a protein-encoding function. Nucleic acid molecules may also be used in methods to ablate or attenuate the expression of a gene in a host cell using gene targeting and knock-out techniques. Suitable nucleic acids also include fragments or variants. Nucleic acid variants include nucleic acids with one or more nucleotide additions, deletions, substitutions, including transitions and transversions, insertion, or modifications (e.g., via RNA or DNA analogs). Alterations may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either

individually among the nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence.

In certain embodiments, the nucleic acids are identical to the sequences represented as SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13 or SEQ ID NO:15. In other embodiments, the nucleic acids may be least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13 or SEQ ID NO:15. Sequence identity calculations can be performed using computer programs, hybridization methods, or calculations. Exemplary computer program methods to determine identity and similarity between two sequences include, but are not limited to, the GCG program package, BLASTN, BLASTX, TBLASTX, and FASTA. The BLAST programs are publicly available from NCBI and other sources. For example, nucleotide sequence identity can be determined by comparing a query sequences to sequences in publicly available sequence databases (NCBI) using the BLASTN2 algorithm.

Embodiments of the nucleic acids include those that encode a polypeptide having the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14 and SEQ ID NO:16, or functional equivalents thereof. A functional equivalent includes fragments or variants that exhibit the ability to function as a signal sequence and direct the extracellular secretion of proteins. As a result of the degeneracy of the genetic code, many nucleic acid sequences can encode a polypeptide having the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14 and SEQ ID NO:16. Such functionally equivalent variants are contemplated herein.

Altered or variant nucleic acids can be produced by one of skill in the art using the sequence data illustrated herein and standard techniques known in the art. Variant nucleic acids may be detected and isolated by hybridization under high stringency conditions or moderate stringency conditions, for example, which are chosen to prevent hybridization of nucleic acids having non-complementary sequences. “Stringency conditions” for hybridizations is a term of art that refers to the conditions of temperature and buffer concentration that permit hybridization of a particular nucleic acid to another nucleic acid in which the first nucleic acid may be perfectly complementary to the second, or the first and second may share some degree of complementarity that is less than perfect. For example, conditions for nucleic acid hybridizations are explained in F. M. Ausubel et al. (eds), 1995, *Current Protocols in Molecular Biology*, John Wiley and Sons, Inc., New York, N.Y., the teachings of which are hereby incorporated by reference.

Nucleic acids may be derived from a variety of sources including DNA, cDNA, synthetic DNA, synthetic RNA, or combinations thereof. Such sequences may comprise genomic DNA, which may or may not include naturally occurring introns. Moreover, such genomic DNA may be obtained in association with promoter regions or poly (A) sequences. The sequences, genomic DNA, or cDNA may be obtained in any of several ways. Genomic DNA can be extracted and purified from suitable cells by means well known in the art. Alternatively, mRNA can be isolated from a cell and used to produce cDNA by reverse transcription or other means.

Oligonucleotides that are fragments of the nucleotide sequences disclosed herein and antisense nucleic acids that are complementary, in whole or in part, to the nucleotide sequences disclosed herein are contemplated herein. Oligonucleotides may be used as primers or probes or for any other use known in the art. Antisense nucleic acids may be used, for example, to inhibit gene expression when introduced into a cell or for any other use known in the art. Oligonucleotides and antisense nucleic acids can be produced by standard techniques known in the art.

Also disclosed herein are recombinant vectors, including expression vectors, containing a gene expressing a histidine kinase, sigma-54 modulation protein, Dxs enzyme, component of a membrane-bound efflux transport system, or TetR family repressor (e.g., SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13 or SEQ ID NO:15 or homologs thereof). A "recombinant vector" is a nucleic acid molecule that is used as a tool for manipulating a nucleic acid sequence of choice or for introducing such a nucleic acid sequence into a host cell. A recombinant vector may be suitable for use in cloning, sequencing, or otherwise manipulating the nucleic acid sequence of choice, such as by expressing or delivering the nucleic acid sequence of choice into a host cell to form a recombinant cell. Such a vector typically contains heterologous nucleic acid sequences not naturally found adjacent to a nucleic acid sequence of choice, although the vector can also contain regulatory nucleic acid sequences (e.g., promoters, untranslated regions) that are naturally found adjacent to the nucleic acid sequences of choice or that are useful for expression of the nucleic acid molecules.

A recombinant vector can be either RNA or DNA, either prokaryotic or eukaryotic, and typically is a plasmid. The vector can be maintained as an extrachromosomal element (e.g., a plasmid) or it can be integrated into the chromosome of a recombinant host cell. The entire vector can remain in place within a host cell, or under certain conditions, the plasmid DNA can be deleted, leaving behind the nucleic acid molecule of choice. An integrated nucleic acid molecule can be under chromosomal promoter control, under native or plasmid promoter control, or under a combination of several promoter controls. Single or multiple copies of the nucleic acid molecule can be integrated into the chromosome. A recombinant vector can contain at least one selectable marker.

The term "expression vector" refers to a recombinant vector that is capable of directing the expression of a nucleic acid sequence that has been cloned into it after insertion into a host cell or other (e.g., cell-free) expression system. A nucleic acid sequence is "expressed" when it is transcribed to yield an mRNA sequence. In most cases, this transcript will be translated to yield an amino acid sequence. The cloned gene is usually placed under the control of (i.e., operably linked to) an expression control sequence. The phrase "operatively linked" refers to linking a nucleic acid molecule to an expression control sequence in a manner such that the molecule can be expressed when introduced (i.e., transformed, transduced, transfected, conjugated or conducted) into a host cell.

Recombinant vectors and expression vectors may contain one or more regulatory sequences or expression control sequences. Regulatory sequences broadly encompass expression control sequences (e.g., transcription control sequences or translation control sequences), as well as sequences that allow for vector replication in a host cell. Transcription control sequences are sequences that control the initiation, elongation, or termination of transcription. Suitable regulatory sequences include any sequence that can function in a host cell or organism into which the recombinant nucleic acid

molecule is to be introduced, including those that control transcription initiation, such as promoter, enhancer, terminator, operator and repressor sequences. Additional regulatory sequences include translation regulatory sequences, origins of replication, and other regulatory sequences that are compatible with the recombinant cell (see, e.g., D. V. Goeddel, *Methods Enzymol.* 185:3-7). The expression vectors may contain elements that allow for constitutive expression or inducible expression of the protein or proteins of interest. For example, vectors comprising the Ptac promoter allow for constitutive expression in the absence of the *lac* gene, but expression may be induced by the addition of isopropyl- β -D-thiogalactopyranoside (IPTG) when the vector also contains the *lac* gene. Numerous inducible and constitutive expression systems are known in the art.

Several regulatory elements (e.g., promoters and terminators) have been isolated and shown to be effective in the transcription and translation of heterologous proteins in the various hosts. Such regulatory regions, methods of isolation, manner of manipulation, etc. are known in the art. To obtain expression in eukaryotic cells, terminator sequences, polyadenylation sequences, and enhancer sequences that modulate gene expression may be required. Sequences that cause amplification of the gene may also be desirable. Suitable promoters include the Ptac, PBAD, PGAP, P_{Eno} or PP_{dc} promoters, among others. Suitable terminators include the T1T2 and T7 terminators, among others.

Expression and recombinant vectors may contain a selectable marker, a gene encoding a protein necessary for survival or growth of a host cell transformed with the vector. The presence of this gene allows growth of only those host cells that express the vector when grown in the appropriate selective media. Typical selection genes encode proteins that confer resistance to antibiotics or other toxic substances, complement auxotrophic deficiencies, or supply critical nutrients not available from a particular media. Markers may be an inducible or non-inducible gene and will generally allow for positive selection. Non-limiting examples of selectable markers include the ampicillin resistance marker (i.e., beta-lactamase), tetracycline resistance marker, neomycin/kanamycin resistance marker (i.e., neomycin phosphotransferase), dihydrofolate reductase, glutamine synthetase, and the like. The choice of the proper selectable marker will depend on the host cell, and appropriate markers for different hosts as understood by those of skill in the art.

Suitable expression vectors may include (or may be derived from) plasmid vectors that are well known in the art, such as those commonly available from commercial sources. Vectors can contain one or more replication and inheritance systems for cloning or expression, one or more markers for selection in the host, and one or more expression cassettes. The inserted coding sequences can be synthesized by standard methods, isolated from natural sources, or prepared as hybrids. Ligation of the coding sequences to transcriptional regulatory elements or to other amino acid encoding sequences can be carried out using established methods. A large number of vectors, including bacterial, yeast, and mammalian vectors, have been described for replication and/or expression in various host cells or cell-free systems, and may be used with the nucleic acid sequences described herein for simple cloning or protein expression.

Suitable expression vectors also include pZB188, pFlag-CTC, or p25143 or other vectors comprising the Ptac, PBAD, PGAP, P_{Eno} or PP_{dc} promoters. In certain embodiments, an expression vector may include an expression cassette comprising a promoter, gene and terminator sequence.

It will be appreciated by one skilled in the art that use of recombinant DNA technologies can improve control of expression of transformed nucleic acid molecules by manipulating, for example, the number of copies of the nucleic acid molecules within the host cell, the efficiency with which those nucleic acid molecules are transcribed, the efficiency with which the resultant transcripts are translated, and the efficiency of post-translational modifications. Additionally, the promoter sequence might be genetically engineered to improve the level of expression as compared to the native promoter. Recombinant techniques useful for controlling the expression of nucleic acid molecules include, but are not limited to, integration of the nucleic acid molecules into one or more host cell chromosomes, addition of vector stability sequences to plasmids, substitutions or modifications of transcription control signals (e.g., promoters, operators, enhancers), substitutions or modifications of translational control signals (e.g., ribosome binding sites), modification of nucleic acid molecules to correspond to the codon usage of the host cell, and deletion of sequences that destabilize transcripts.

The nucleic acids, including parts or all of expression vectors, may be isolated directly from cells, or, alternatively, the polymerase chain reaction (PCR) method can be used to produce the nucleic acids. Primers used for PCR can be synthesized using the sequence information provided herein and can further be designed to introduce appropriate new restriction sites, if desirable, to facilitate incorporation into a given vector for recombinant expression. The nucleic acids can be produced in large quantities by replication in a suitable host cell (e.g., prokaryotic or eukaryotic cells such as bacteria, yeast, insect or mammalian cells). The production and purification of nucleic acids are described, for example, in Sambrook et al., 1989; F. M. Ausubel et al., 1992, *Current Protocols in Molecular Biology*, J. Wiley and Sons, New York, N.Y.

The nucleic acids described herein may be used in methods for production of proteins or polypeptides through incorporation into cells, tissues, or organisms. In some embodiments, a nucleic acid encoding all or part of ZMO1162 (SEQ ID NO:2) or ZMO0038 (SEQ ID NO:4) or any other amino acid sequence disclosed herein, or a functional fragment thereof, may be incorporated into a vector for expression of the encoded polypeptide in suitable host cells. The vector may then be introduced into one or more host cells by any method known in the art. One method to produce an encoded protein includes transforming a host cell with one or more recombinant nucleic acids (such as expression vectors) to form a recombinant cell. The term "transformation" is generally used herein to refer to any method by which an exogenous nucleic acid molecule (i.e., a recombinant nucleic acid molecule) can be inserted into a cell, but can be used interchangeably with the term "transfection."

Non-limiting examples of suitable host cells include bacteria, archaea, insect, fungi (e.g., yeast), plant, and animal cells (e.g., mammalian). Specific examples include *Zymomonas mobilis*, *Escherichia coli*, *Bacillus subtilis*, and *Saccharomyces cerevisiae*. Host cells can be either untransfected cells or cells that are already transfected with at least one other recombinant nucleic acid molecule.

Host cells can be transformed, transfected, or infected as appropriate by any suitable method including electroporation, calcium chloride-, lithium chloride-, lithium acetate/polyethylene glycol-, calcium phosphate-, DEAE-dextran-, liposome-mediated DNA uptake, spheroplasting, injection, microinjection, microprojectile bombardment, phage infection, viral infection, or other established methods. Alternatively, vectors containing the nucleic acids of interest can be

transcribed in vitro, and the resulting RNA introduced into the host cell by well-known methods, for example, by injection (see, Kubo et al., FEBS Letts. 241:119). Exemplary embodiments include a host cell or population of cells expressing one or more nucleic acid molecules or expression vectors described herein (for example, a genetically modified microorganism). The cells into which nucleic acids have been introduced as described above also include the progeny of such cells.

Host cells carrying an expression vector (i.e., transformants or clones) may be selected using markers depending on the mode of the vector construction. The marker may be on the same or a different DNA molecule. In prokaryotic hosts, the transformant may be selected, for example, by resistance to ampicillin, tetracycline or other antibiotics. Production of a particular product based on temperature sensitivity may also serve as an appropriate marker.

Biocatalyst microorganisms may be cultured in an appropriate fermentation medium. An appropriate, or effective, fermentation medium refers to any medium in which a microorganism, when cultured, is capable of expressing polypeptides, catalyzing the production of sugars from lignocellulosic biomass, or fermenting sugars to biofuels. Such a medium is typically an aqueous medium comprising assimilable carbon, nitrogen and phosphate sources, but can also include appropriate salts, minerals, metals and other nutrients. Microorganisms and other cells can be cultured in conventional fermentation bioreactors and by any fermentation process, including batch, fed-batch, cell recycle, and continuous fermentation. The pH of the fermentation medium is regulated to a pH suitable for growth and protein production of the particular organism. The fermentor can be aerated in order to supply the oxygen necessary for fermentation and to avoid the excessive accumulation of carbon dioxide produced by fermentation. Culture media and conditions for various host cells are known in the art. Exemplary conditions for the culture of bacteria such as *Z. mobilis* can be found, for example, in Senthilkumar et al., Arch. Microbiol. 191:529-41 and Arfman et al., J. Bacteriol. 174:7370-8.

As used herein, the terms "protein" and "polypeptide" are synonymous. "Peptides" are defined as fragments or portions of polypeptides, preferably fragments or portions having at least one functional activity as the complete polypeptide sequence. "Isolated" proteins or polypeptides are proteins or polypeptides purified to a state beyond that in which they exist in cells. In certain embodiments, they may be at least 10% pure; in others, they may be substantially purified to 80% or 90% purity or greater. Isolated proteins or polypeptides include essentially pure proteins or polypeptides, proteins or polypeptides produced by chemical synthesis or by combinations of biological and chemical methods, and recombinant proteins or polypeptides that are isolated. Proteins or polypeptides referred to herein as "recombinant" are proteins or polypeptides produced by the expression of recombinant nucleic acids.

Proteins or polypeptides encoded by nucleic acids as well as functional portions or variants thereof are also described herein. Polypeptide sequences may be identical to the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14 and SEQ ID NO:16, or may include up to a certain integer number of amino acid alterations. Such protein or polypeptide variants retain functionality (e.g., as histidine kinases, sigma-54 modulation proteins, Dxs enzymes, components of a membrane-bound efflux transport system, or TetR family repressors), and include mutants differing by the addition, deletion or substitution of one or more amino acid

residues, or modified polypeptides and mutants comprising one or more modified residues. The variant may have one or more conservative changes, wherein a substituted amino acid has similar structural or chemical properties (e.g., replacement of leucine with isoleucine). Alterations may occur at the amino- or carboxy-terminal positions of the reference polypeptide sequence or anywhere between those terminal positions, interspersed either individually among the amino acids in the reference sequence or in one or more contiguous groups within the reference sequence.

In certain embodiments, the polypeptides may be at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14 and SEQ ID NO:16 and possess one or more functions ascribed to the polypeptide (e.g., histidine kinase, sigma-54 modulation, Dxs enzyme, membrane-bound efflux transport, or TetR family repressor activity). Percent sequence identity can be calculated using computer programs (such as the BLASTP and TBLASTN programs publicly available from NCBI and other sources) or direct sequence comparison. Polypeptide variants can be produced using techniques known in the art including direct modifications to isolated polypeptides, direct synthesis, or modifications to the nucleic acid sequence encoding the polypeptide using, for example, recombinant DNA techniques.

Modified polypeptides, including those with post-translational modifications, are also contemplated herein. Isolated polypeptides may be modified by, for example, phosphorylation, methylation, farnesylation, carboxymethylation, geranyl geranylation, glycosylation, acetylation, myristoylation, prenylation, palmitation, amidation, sulfation, acylation, or other protein modifications. They may also be modified with a label capable of providing a detectable signal, either directly or indirectly, including, but not limited to, radioisotopes and fluorescent compounds. The polypeptides may be useful as antigens for preparing antibodies by standard methods. Monoclonal and polyclonal antibodies that specifically recognize the polypeptides disclosed herein are contemplated.

Polypeptides may be retrieved, obtained, or used in "substantially pure" form, a purity that allows for the effective use of the protein in any method described herein or known in the art. For a protein to be useful in any of the methods described herein or in any method utilizing enzymes of the types described herein, it is substantially free of contaminants, other proteins and/or chemicals that might interfere or that would interfere with its use in the method (e.g., that might interfere with enzyme activity), or that at least would be undesirable for inclusion with a protein.

The biocatalyst organisms described herein may be used to ferment simple sugars directly to biofuels. The organisms are contacted with the sugars in a fermentation broth under conditions suitable for fermenting the sugars to biofuels. Fermentation conditions vary with the organism, feedstock or sugar used, or with the desired biofuel product, and can be determined by those skilled in the art. For the fermentation of acid pretreated corn stover hydrolysate to ethanol using a strain of *Zymomonas*, for example, conditions may be those set forth in Example 1 below.

The biocatalyst organisms described herein may also be used as part of an integrated process to derive biofuels from raw biomass or cellulosic materials. Typically, raw cellulosic biomass material is pretreated in order to convert, or partially convert, cellulosic and hemicellulosic components into enzymatically hydrolyzable components (e.g., oligosaccharides). The pretreatment process may also serve to separate the cel-

lulosic and hemicellulosic components from solid lignin components also present in the raw cellulosic material. The pretreatment process typically involves reacting the raw cellulosic biomass material, often as a finely divided mixture or slurry in water, with an acid, such as sulfuric acid. The pretreated biomass may then be treated with a saccharification step in which oligosaccharides are enzymatically hydrolyzed into simple sugars. The free sugars or oligosaccharides produced in the saccharification step are then subjected to fermentation conditions for the production of a biofuel. Fermentation can be accomplished by combining one or more biocatalyst microorganisms with the produced sugars under conditions suitable for fermentation.

Methods for breaking down lignocellulose and lignocellulose-containing biomass are also disclosed herein. Biocatalysts containing the genetic modifications described herein or additional modifications that aid in the breakdown of lignocellulose may be brought into contact with a lignocellulose-containing biomass (for example, by culturing the organism in the presence of the lignocellulose-containing biomass) in the presence of cellulolytic or oligosaccharide degrading enzymes to result in its degradation. Treated biomass is typically degraded into simpler forms of carbohydrates, and in some cases glucose, which may then be used in the formation of ethanol or other industrial chemicals, as is known in the art. Biomass degradation may be achieved by culturing a microorganism in media supplemented with a source of lignocellulose-containing biomass, in addition to media components necessary for growth of the microorganism. In addition to the use of lignocellulose-containing biomass as an energy source for the host, the growth media may need to be supplemented with additional components including, but not limited to, yeast extract. Multiple enzymes may be needed to utilize lignocellulose-containing biomass as a primary source of energy. Such enzymes may be expressed by one or more microorganism, or purified enzymes or mixtures of enzymes may be directly added to the culture. For example, endoglucanase, exoglucanase, and β -glucosidase activities may be required to fully degrade cellulosic materials into fermentable sugars. These enzymatic activities can arise from individual enzymes, or in some cases, multiple types of cellulolytic activity can arise from the same enzyme. Further, there are different enzymatic activities that can substitute for other activities. For instance, processive endoglucanases can have overlapping roles with exoglucanases.

Lignocellulose-containing biomass may be derived from any source known in the art, and may be degraded to oligosaccharides and simple sugars using enzymes or chemicals. Biofuels such as ethanol may be subsequently produced from the fermentation of sugars derived from the cellulosic materials. Examples include bioenergy crops, agricultural residues, municipal solid waste, industrial solid waste, sludge from paper manufacture, yard waste, wood and forestry waste. Examples of biomass include, but are not limited to, corn grain, corn cobs, crop residues such as corn husks, corn stover, corn fiber, grasses, wheat, wheat straw, barley, barley straw, hay, rice straw, switchgrass, waste paper, sugar cane bagasse, sorghum, soy, components obtained from milling of grains, trees, branches, roots, leaves, wood (e.g., poplar) chips, sawdust, shrubs and bushes, vegetables, fruits, flowers and animal manure. Biomass samples may be processed or pretreated using known methods prior to or after degradation. Examples of pretreatment methods can be found, for example, in Galbe et al., *Adv Biochem Eng Biotechnol.*; 108:41-65.

A lignocellulosic biomass or other cellulosic feedstock may be subjected to pretreatment at an elevated temperature

in the presence of water, a dilute acid, concentrated acid or dilute alkali solution for a time sufficient to at least partially hydrolyze the hemicellulose components before subsequent enzymatic treatment or fermentation to biofuels. Additional suitable pretreatment regimens include ammonia fiber expansion (AFEX), treatment with hot water or steam, or lime pretreatment.

The resulting products after cellulose degradation and fermentation may be isolated or purified. After fermentation, for example, a biofuel may be separated from the fermentation broth by any conventional technique known to separate alcohol from aqueous solutions, including evaporation, distillation, solvent extraction and membrane separation. Solids such as microorganisms may be removed before separation to enhance separation efficiency. Fermentation products may also be converted to products other than ethanol. Examples include conversion to higher alcohols, hydrocarbons, or other advanced fuels via biological or chemical pathways, or combination thereof.

EXAMPLES

Example 1

The following materials and methods were used in the Examples that follow:

Construction of the Overexpression Mutant Library

A transposon insertion system (Epicentre Biotechnologies, Madison, Wis.) was used to generate transposomes for the transposition. For the construction of “Super Pgap” overexpression mutant library (OEL), the “Super Pgap” promoter was cloned into an integrative plasmid (pMOD2Splox), and the fragment digested with PvuII containing ME-loxP-Pgap-Sp-loxP-ME was gel purified and treated with transposases, in 16-20% glycerol at room temperature for 30 minutes before the electroporation transformation. Transformants were selected on RMG2Sp200 plates, and the colonies were collected.

Enrichment of 33C Overexpression Mutant Library in Selective Media

Frozen library vials were thawed and revived before spreading on selective media including RMA2 broth and plate, RMG plate with arabitol, and 40% hydrolysate plates. Colonies with large size were selected for continuous adaptation on the selective conditions.

Overexpression of Genes Related to Inhibitor Tolerance in 33C and 8b Background

Overexpression constructs for genes related to pretreatment inhibitor tolerance, which were identified from transcriptomics studies under Hydrolysate Toxicity subtask, were transformed into 33C and 8b.

Inhibitor Tolerance and Non-Native Sugar Utilization Evaluation

Strains were revived from overnight culture with OD_{600nm} adjusted to 1.5 using RM-, 10 μL seed culture was added into 300 μL media with an initial OD_{600nm} about 0.05. Bioscreen assay was conducted at 33° C. without shaking.

Sequencing

Zymomonas genomic DNA samples were prepared from overnight cultures using Qiagen’s DNeasy Blood & tissue Kit. Genomic DNA was extracted and sequenced using primers 126604-F and 126604-R, and the insertional location was identified through sequencing analysis.

Fermentation of Acid Pretreated Corn Stover

Rich medium (RM) consisting of 10 g/L yeast extract and 2 g/L KH₂PO₄ was added to neutralized saccharified whole slurry, and the fermentation were performed in BioStat-Q

Plus fermentors at a 300-mL working volume with an initial inoculum at an OD_{600 nm} value of approximately 1.0 with pH controlled to 5.8 with 4M KOH at 33° C., 300 rpm.

RNA Extraction, cDNA Synthesis, and qRT-PCR

Total RNA was extracted from cell pellets growing in RMG5 or RMX5 resuspended in TRIzol reagent (Invitrogen, CA). Each total RNA preparation was treated with RNase-free DNase I (Ambion, TX) to digest residual genomic DNA and subsequently purified using the RNeasy Mini Kit (Qiagen, CA). Total cellular RNA was quantified with a NanoDrop ND-1000 spectrophotometer (NanoDrop Technologies, DE) and RNA quality was assessed with Agilent Bioanalyzer (Agilent, CA). Purified RNA of high quality was used as the template to generate cDNA using Bio-Rad iScript cDNA Synthesis Kit (Bio-Rad, CA). cDNA was then used as template for qRT-PCR using Bio-Rad iQ SYBR Green supermix with a Bio-Rad CFX96 Touch Real-Time PCR Detection System (Bio-Rad, CA).

Chemical Analysis

Concentrations of ethanol, HMF, furfural, lactic acid, glycerol and acetic acid present in hydrolyzates were determined from filtered sample supernatants that were analyzed by high performance liquid chromatography (HPLC) Agilent1100 series (Agilent, CA) utilizing a BioRad HPX-87H organic acids column and Cation H⁺ guard cartridge (Bio-Rad, CA) operating at 55° C. A refractive index detector was used for compound detection. Dilute sulfuric acid (0.01 N) was used as the isocratic mobile phase at a flow rate of 0.6 ml min⁻¹. Analysis of furfural conversion products was performed on a C-18 column starting with 10% acetonitrile as the mobile phase at a flow rate of 0.5 mL/min and ending with 90% acetonitrile over a 35 minute gradient.

Example 2

Selection of Biocatalysts Tolerant to Hydrolysate

A transposon-based overexpression construct was created and used to build a mutant library of *Z. mobilis*. A library of a randomly integrated strong promoters (“Super Pgap”) throughout the genome of an arabinose utilizing *Zymomonas* strain (33C; an engineered strain capable of utilizing glucose, xylose, and arabinose) was generated. This library was screened to identify mutants with increased ability to tolerate hydrolysate—about 30,000 mutant isolates were pooled and hydrolysate-tolerant candidates were selected on agar plates containing 40% pretreated corn stover hydrolysate. Five candidates from the over-expression library exhibiting improved growth in the presence of 40% hydrolysate were selected by continuously transferring the single colony onto 40% hydrolysate agar plate eight times to stabilize the phenotype of hydrolysate tolerance. These five candidates are shown in FIG. 9.

A Bioscreen (Growth Curves USA, Piscataway, N.J.) high-throughput growth assay was used to characterize the phenotypic changes associated with these five mutant strains in the presence of different sugar sources (glucose, xylose or arabinose) with the supplementation of the major hydrolysate inhibitors (acetate, furfural, and the end-product ethanol). The assay results indicated that while the mutant and parent strains grow equally well in the absence of an inhibitor (FIG. 10A), the five mutants had enhanced furfural tolerance and increased ethanol tolerance relative to their parental strain 33C in Rich Media supplemented with 2% (w/v) glucose (RMG2) (FIGS. 10B and C). Therefore, these five candidate strains had improved hydrolysate tolerance from their enhanced ethanol and/or furfural tolerance capabilities compared to parental strain 33C.

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An agar plate assay also indicated that these strains had enhanced furfural tolerance (FIG. 11). In the absence of furfural, the mutant strains had growth characteristics similar to that of the parental 33C strain (FIG. 11A). On the same plates supplemented with furfural, the mutant strains performed much better than 33C (FIG. 11B-D). As shown in FIGS. 11C and 11D, this result is particularly evident at higher furfural concentrations (3-4 g/L).

Example 3

Genetic Modifications in Hydrolysate Tolerant Biocatalysts

Genomic DNA was extracted and subjected to chromosomal sequencing to determine the insertional location of the promoter construct in each mutant and the genes affected by the insertion. Sequencing results indicated that the mutant designated OEL22 inserted into the upstream region of ZMO1162 gene (encoding a histidine kinase, PhoR homolog). The mutants designated OEL19, OEL23, OEL26, and OEL31 each inserted into ZMO0038 gene (encoding a Sigma 54 modulation protein), with OEL 31 inserted 16-bp downstream of the OEL19 insertion site. The insertions of OEL19, 23, 26, and 31 most likely cause the disruption of gene ZMO0038 by insertional deletion, and OEL22 may result in the over-expression ZMO1162/PhoR.

PCR primers were designed to amplify the regions covering the mutated regions of mutants OEL19 and OEL22. Using primer sets of OEL19_F (CCGTCCTTCCAATTCGATAA; SEQ ID NO:17) and OEL19_R (CCCCAATATGACCGAATCAC; SEQ ID NO:18) for OEL19 and OEL22_F (ATCGGCAATCATCAGGAAAG; SEQ ID NO:19) and OEL22_R (ATACCATCGCCTTCATCTGC; SEQ ID NO:20) for OEL22, the resulting PCR products (about 4.2 kb) containing portions up- and down-stream of the insertion sites were purified and electroporated into 33C or 8b competent cells to replace wild-type DNA nucleotide sequences with mutant version of OEL19 and OEL33 respectively. Four mutant strains were therefore constructed, designated 8b-OEL19, 8b-OEL22, 33C-OEL19 and 33C-OEL22. The transformants were confirmed by Sanger sequencing.

The resulting strains and the parent strains 33C and 8b were subjected to the hydrolysate plate assay as described in Example 2 and FIG. 9. The results of this assay indicate that the 8b-OEL19, 8b-OEL22, 33C-OEL19 and 33C-OEL22 strains exhibited an enhanced hydrolysate tolerance of about 100- to 1,000-fold relative to the parent stains 33C and 8b (FIG. 12).

Example 4

Z. Mobilis 8b Knockout Library Construction and Screening

A transposition vector containing the spectinomycin resistant gene marker (pMOD2SpLoxP) flanked by loxP sites and transposable mosaic ends was used for the construction of a knockout library in *Z. mobilis* 8b by randomly inserting the DNA containing spectinomycin marker into the chromosome and/or native plasmid using transposase. The linear fragment from SCS110/pMOD2SpLoxP was prepared by digestion with PvuII followed by gel purification. Multiple transposon reactions containing 200 ng of the linear fragment with 2 μ L 80% glycerol and 4 μ L transposase was incubated at room temperature for 30 minutes, followed by electroporation into electrocompetent *Z. mobilis* 8b. Cells were outgrown without antibiotics for 6 hours at 30° C. in MMG (50 g/L glucose, 10 g/L yeast extract, 5 g/L tryptone, 2.5 g/L (NH₄)₂SO₄ and 0.2 g/L K₂HPO₄) and 100 mM MgSO₄, followed by plating on MMG plates containing 200 ng/mL spectinomycin. Thirty-

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eight plates containing approximately 600 colonies per plate (20,200 colonies total) were scraped from plates and grown in RMGSp200 for several generations prior to being preserved as glycerol stocks.

Both *Z. mobilis* 8b and 8b knockout library cultures were revived from glycerol stocks in 20 mL MRMG0.75x0.25 (10 g/L yeast extract, 2 g/L KH₂PO₄ and 1 g/L MgSO₄.7H₂O, 7.5 g/L glucose and 2.5 g/L xylose) and also containing 200 ng/mL spectinomycin for 1.5 hours at 35° C., 125 rpm. Cells were centrifuged and resuspended to a final OD_{600 nm} of 0.025 in a 100 mL culture, and grown for an additional 3-4 generations at 35° C. in 125 mL Erlenmeyer flasks with foam enclosures, 125 rpm (about 6 hours). Cells were initially screened on MRMGS (5% w/v glucose) plates containing 0, 3, 5, or 7.5 g/L of furfural, equivalent to MICs of 0.75x, 1x or 1.5x. MIC 1x is the minimum (lowest) concentration of inhibitor needed for complete inhibition of growth (RMG2) over a 24-hour period. Approximately 500, 1000 and 2000 colonies were plated in triplicates. Furfural levels were also tested at 0.7, 1.5, 3 or 4 g/L in glucose.

The agar plate dilution method was used to compare furfural tolerance among mutants which involved growing cultures to log phase in RMG2, then preparing 5-fold dilutions in microtiter plates. Using a 48-pin replicator, cells were replica plated onto RMG agar plates containing 0 or 3 g/L furfural and incubated anaerobically in chambers at 33° C. for 1 to 5 days.

Example 5

Growth and Fermentation Assays

For growth assays in sugars and furfural, *Z. mobilis* 8b was revived from frozen glycerol stocks for about 6-8 hours in 10 mL of RMG2 (2% glucose) at 33° C. Bioscreen C assays were carried out as described above. Cells were inoculated into Bioscreen C wells containing a total volume of 300 μ L and incubated without shaking at 33° C. at an initial density of OD_{600 nm} of 0.05 (approximately 5x10⁶ cells/mL). Turbidity measurements (OD_{420-580 nm}) were taken every 10 minutes for up to 48 hours.

For pH controlled fermentation of *Z. mobilis* 8b in furfural, six fermentors (300 mL volume) were inoculated at an optical density OD_{600 nm}=0.1 with *Z. mobilis* 8b in RMG8 (10 g/L yeast extract, 2 g/L KH₂PO₄ and 8% (w/v) glucose) with 0, 1, 2, 3, 4 or 5 g/L furfural, 33° C., pH of 6.0 controlled with 2M KOH. Fermentors were sparged with filter-sterilized nitrogen gas prior to fermentation. Samples were taken periodically to monitor cell densities, sugars, furfural and ethanol concentrations.

Example 6

Analysis of Mutants

From the preliminary screening of the knockout library described in Example 4, 34 colonies were isolated and evaluated for their growth in RMG2 containing 3 g/L furfural using Bioscreen C. Slight improvement in growth was observed (up to 20%) over the original 8b strain. Chromosomal sequencing of the insertion site revealed that two of the isolates had insertion sites within the same gene (ZMO1598) but at two different locations. ZMO1598 encodes for a 1-deoxy-D-xylose-5-phosphate synthase (Dxs), an enzyme involved in several different pathways. There is also another gene ZMO1234, which also encodes for Dxs that is nearly identical to gene product of ZMO1598 present in *Z. mobilis* except for the protein amino and carboxyl terminus.

From a larger plate screening on 4 g/L furfural, 39 colonies were isolated, which were further screened on plates using the agar plate dilution method. An additional 51 colonies from the 3 g/L furfural plate screening were also tested. The majority of isolates were more viable at higher dilutions. Selected isolates from 3 and 4 g/L furfural screens were further tested in Bioscreen C growth assays in the presence of furfural; however, slight improvement was only noted (approximately 10-30%) at the 3 g/L furfural level and not at the lower concentrations.

Since two of the previous furfural tolerant spectinomycin (spec) mutants had insertions in *dxs*, it was possible this gene knockout was present in the remaining furfural isolates. Chromosomal DNA from isolates was tested for spec insertions in ZMO1598 and ZMO1234 by sequencing PCR products using primers homologous to the *dxs* gene. From 98 isolates, 29 were positive for insertions into ZMO1598 and 2 from ZMO1234. Furthermore, insertions were present in 13 different locations within the gene ZMO1598 and 2 within the gene ZMO1234. The mutations account for approximately 30% of the isolates tolerant to furfural and indicate a high likelihood that knockout of these genes is responsible for the observed phenotype.

Using homologous recombination with linear DNA obtained by PCR of spec insertion of four isolates into native *Z. mobilis* 8b, four new mutants were tested and compared with knockout library isolates for furfural tolerance using the plate assay on 3 g/L furfural. As shown in FIG. 13, knockouts within the same genes of ZMO1598 and ZMO1234 in the original 8b strain had similar tolerance to furfural as the original isolate, confirming that the gene knockout, not adaptation, was responsible for the observed phenotype.

Chromosomal DNA from the remaining isolates that were not identified as ZMO1598 and ZMO1234 mutants were

sequenced. Out of the 56 isolates sequenced, the majority of knockouts (44), had spectinomycin insertions within the operon containing the genes, ZMO0282, ZMO0283 and ZMO0285. There were 11 isolates with knockouts within the gene ZMO0282 at 6 different insertion sites, 19 within ZMO0283 at 12 unique insertion sites and 14 within ZMO0285 at 3 different insertion sites.

ZMO0282 has similarity to the *acrA* gene of *E. coli* and is a membrane fusion protein, part of a multi-drug efflux transport system, along with the *acrB* gene, an inner-membrane associated proton-substrate antiporter. It functions as a part of the AcrAB/TolC multidrug-efflux complex. The purpose of this system is for the extrusion of toxic chemicals. ZMO0285 has homology to the *cusC* gene of *E. coli*, which is an outer membrane porin, part of a copper/silver efflux transport system. Most likely it acts like TolC as the outer membrane protein, associating with ZMO0282 and ZMO0283. This analysis demonstrates that disrupting ZMO1598 and/or ZMO1234 as well as the operon containing ZMO0282, ZMO0283 and ZMO0285 conferred furfural resistance in *Zymomonas*. The great number of independent insertion events in these locations strongly suggested that these two hot spots for gene disruption create the observed furfural tolerant phenotype on agar plates, which was subsequently confirmed by constructing the knockout phenotypes in a clean 8b background. Also, a TetR family repressor gene ZMO0281 (which may be a potential repressor for the operon containing ZMO0282, ZMO0283 and ZMO0285) was upregulated during furfural challenge. Furthermore, overexpression of ZMO0281 also confirmed the improved furfural resistance in *Zymomonas*. These results demonstrate that either knockout of the expression of ZMO0282, ZMO0283 or ZMO0285 or downregulation of the expression of ZMO0282, ZMO0283 or ZMO0285 through the overexpression of the repressor confers furfural resistance.

SEQUENCE LISTING

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Tyr Pro Phe Ser Gln Ala Thr Ala Ala Asp Ile Ile Ile Ala Met Asp
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Glu Pro Ala Leu Leu Val Asn Gln Gly Gln Val Glu Val Ala Asn Arg
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Ala Ala Glu Asn Leu Leu Gly Met His Ile Glu Gly Gly Asp Ile Arg
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Gly Leu Met Asp Asp Gly Leu Lys Ile Arg Thr Leu Arg Leu Pro Asp
595 600 605

Arg Phe Gln Pro Gln Asp Lys Gln Glu Arg Gln Tyr Ala Glu Ala Gly
610 615 620

Leu Asp Ala Asp Gly Ile Val Ala Ala Val Thr Ala Ala Leu Gln Arg
625 630 635 640

Asn Ser Lys Pro Val Glu Val Val Glu Leu Thr Thr Lys Val Thr Glu
645 650 655

Asp Met Thr Leu
660

<210> SEQ ID NO 7

<211> LENGTH: 1950

<212> TYPE: DNA

<213> ORGANISM: Zymomonas mobilis

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(1950)

<400> SEQUENCE: 7

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atg ttt ccg aat gac aag acg ccg ctg tta gac aag atc aag aca ccg      48
Met Phe Pro Asn Asp Lys Thr Pro Leu Leu Asp Lys Ile Lys Thr Pro
1           5           10           15

gca gaa ttg cgt caa tta gat cgc aac agc ctc cgg caa ttg gcg gat      96
Ala Glu Leu Arg Gln Leu Asp Arg Asn Ser Leu Arg Gln Leu Ala Asp
20           25           30

gaa tta cgg aaa gag acc atc tcg gca gtg ggt gtg acc ggc gga cat     144
Glu Leu Arg Lys Glu Thr Ile Ser Ala Val Gly Val Thr Gly Gly His
35           40           45

ctc ggt tcc ggt ctg ggg gtt atc gaa tta acg gta gcc ctt cac tat     192
Leu Gly Ser Gly Leu Gly Val Ile Glu Leu Thr Val Ala Leu His Tyr
50           55           60

gtt ttc aac acg ccc aaa gac gct tta gtc tgg gat gtt ggg cat caa     240
Val Phe Asn Thr Pro Lys Asp Ala Leu Val Trp Asp Val Gly His Gln
65           70           75           80

acc tat cct cac aag att tta aca ggt cgc cgc gat cgt att cgg aca     288
Thr Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Asp Arg Ile Arg Thr
85           90           95

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ttg cgg caa cgt gac ggc tta tcg ggc ttt acg cag cgc gcg gag agc	336
Leu Arg Gln Arg Asp Gly Leu Ser Gly Phe Thr Gln Arg Ala Glu Ser	
100 105 110	
gaa tat gac gct ttt gga gcc gcg cat agt tcg act tct att tct gcg	384
Glu Tyr Asp Ala Phe Gly Ala Ala His Ser Ser Thr Ser Ile Ser Ala	
115 120 125	
gcg ctc ggc ttt gcg atg gcc agc aaa tta tcc gac agc gac gac aaa	432
Ala Leu Gly Phe Ala Met Ala Ser Lys Leu Ser Asp Ser Asp Asp Lys	
130 135 140	
gcg gtt gcg att atc ggt gat ggc tcg atg acg gca ggc atg gct tat	480
Ala Val Ala Ile Ile Gly Asp Gly Ser Met Thr Ala Gly Met Ala Tyr	
145 150 155 160	
gaa gcc atg aat aac gcc aag gcg gcg ggt aag cgc ctg att gtc att	528
Glu Ala Met Asn Asn Ala Lys Ala Ala Gly Lys Arg Leu Ile Val Ile	
165 170 175	
ttg aat gac aat gaa atg tcg att tca ccg ccg gtg ggt gcc tta tcg	576
Leu Asn Asp Asn Glu Met Ser Ile Ser Pro Pro Val Gly Ala Leu Ser	
180 185 190	
tct tat ttg agc cgc ctg att tcc tca ccg cct ttc atg aat ttg cgc	624
Ser Tyr Leu Ser Arg Leu Ile Ser Ser Arg Pro Phe Met Asn Leu Arg	
195 200 205	
gat atc atg cgc ggc gtt gtt aac ccg atg cca aaa ggc ttg gca acg	672
Asp Ile Met Arg Gly Val Val Asn Arg Met Pro Lys Gly Leu Ala Thr	
210 215 220	
gct gcc cgc aag gct gat gaa tat gcg cgt ggt atg gca acc ggt ggc	720
Ala Ala Arg Lys Ala Asp Glu Tyr Ala Arg Gly Met Ala Thr Gly Gly	
225 230 235 240	
acc ttc ttt gaa gag ctg ggc ttt tac tat gtt ggc ccc gtg gat ggt	768
Thr Phe Phe Glu Glu Leu Gly Phe Tyr Tyr Val Gly Pro Val Asp Gly	
245 250 255	
cat aat tta gat cag ctc att cca gtt tta gaa aat gtc cgc gat gcc	816
His Asn Leu Asp Gln Leu Ile Pro Val Leu Glu Asn Val Arg Asp Ala	
260 265 270	
aag gac ggc ccc att ttg gtg cat gtc gtc act cgc aaa ggc caa ggc	864
Lys Asp Gly Pro Ile Leu Val His Val Val Thr Arg Lys Gly Gln Gly	
275 280 285	
tat gct ccg gct gaa gcg gcc aag gac aaa tat cac gcc gtg cag cgc	912
Tyr Ala Pro Ala Glu Ala Ala Lys Asp Lys Tyr His Ala Val Gln Arg	
290 295 300	
ttg gat gtg gtt tcc ggt aag cag gcg aaa gcg ccc ccg gga cct ccc	960
Leu Asp Val Val Ser Gly Lys Gln Ala Lys Ala Pro Pro Gly Pro Pro	
305 310 315 320	
agc tat acc tct gtt ttt tcg gaa cag ctg atc aag gaa gct aag caa	1008
Ser Tyr Thr Ser Val Phe Ser Glu Gln Leu Ile Lys Glu Ala Lys Gln	
325 330 335	
gac gat aag att gtg acc att acg gca gct atg ccg act ggc acc ggt	1056
Asp Asp Lys Ile Val Thr Ile Thr Ala Ala Met Pro Thr Gly Thr Gly	
340 345 350	
ctt gat cgt ttt cag caa tat ttt cct gaa aga atg ttt gat gtc ggt	1104
Leu Asp Arg Phe Gln Gln Tyr Phe Pro Glu Arg Met Phe Asp Val Gly	
355 360 365	
att gcc gaa caa cat gcc gta acc ttt gcg gct ggt ttg gcg gct gcc	1152
Ile Ala Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu Ala Ala Ala	
370 375 380	
ggt tac aag cct ttc tgt tgt ctc tat tcg acc ttc ttg cag cgc ggc	1200
Gly Tyr Lys Pro Phe Cys Cys Leu Tyr Ser Thr Phe Leu Gln Arg Gly	
385 390 395 400	
tat gac cag ttg gtg cat gat gtc gct atc cag aat ttg ccg gtg cgc	1248
Tyr Asp Gln Leu Val His Asp Val Ala Ile Gln Asn Leu Pro Val Arg	

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405	410	415	
ttc gcc gtc gat cgt gcg ggt ctt gtc ggt gcc gat ggg gca acc cat Phe Ala Val Asp Arg Ala Gly Leu Val Gly Ala Asp Gly Ala Thr His 420	425	430	1296
gcg ggt agc ttc gac ctc gcc ttt atg gtt aat ctc ccg aat atg gtc Ala Gly Ser Phe Asp Leu Ala Phe Met Val Asn Leu Pro Asn Met Val 435	440	445	1344
gtg atg gcg cct tcc gat gaa cgg gaa ttg gcc aat atg gtg cat agc Val Met Ala Pro Ser Asp Glu Arg Glu Leu Ala Asn Met Val His Ser 450	455	460	1392
atg gcg cat tat gac caa ggc ccg atc tcg gtg cgt tat ccg cgt ggt Met Ala His Tyr Asp Gln Gly Pro Ile Ser Val Arg Tyr Pro Arg Gly 465	470	475	1440
aat ggt gtg ggt gtc tcc ttg gaa ggt gaa aag gaa att ctg cct atc Asn Gly Val Gly Val Ser Leu Glu Gly Glu Lys Glu Ile Leu Pro Ile 485	490	495	1488
ggg aaa ggt cgc ctg atc cgt cgc ggt aaa aag gtt gct atc cta tct Gly Lys Gly Arg Leu Ile Arg Arg Gly Lys Lys Val Ala Ile Leu Ser 500	505	510	1536
ctc ggc act cga ttg gaa gaa tcc ttg aag gct gct gat cgg ctt gat Leu Gly Thr Arg Leu Glu Glu Ser Leu Lys Ala Ala Asp Arg Leu Asp 515	520	525	1584
gct caa ggt ttg tcg aca tcg gtt gct gat atg cgt ttt gct aag ccc Ala Gln Gly Leu Ser Thr Ser Val Ala Asp Met Arg Phe Ala Lys Pro 530	535	540	1632
ttg gat gaa gcg ctg acc cgc caa ctt ttg aaa agc cat cag gtc att Leu Asp Glu Ala Leu Thr Arg Gln Leu Leu Lys Ser His Gln Val Ile 545	550	555	1680
att acc att gaa gaa ggc gct ttg ggt ggt ttt gca acc caa gtc ctg Ile Thr Ile Glu Glu Gly Ala Leu Gly Gly Phe Ala Thr Gln Val Leu 565	570	575	1728
acg atg gct tcg gat gaa ggc ctg atg gat gac gga ttg aaa atc cgc Thr Met Ala Ser Asp Glu Gly Leu Met Asp Asp Gly Leu Lys Ile Arg 580	585	590	1776
acc ctg cgt ctg ccg gat cgg ttc cag ccg caa gac aag caa gaa cgg Thr Leu Arg Leu Pro Asp Arg Phe Gln Pro Gln Asp Lys Gln Glu Arg 595	600	605	1824
caa tat gcc gaa gcc ggt ctt gat gct gat ggc atc gtt gct gcg gtt Gln Tyr Ala Glu Ala Gly Leu Asp Ala Asp Gly Ile Val Ala Ala Val 610	615	620	1872
atc tcc gca ttg cat cgt aat tct aaa ccc gtg gaa gtc gtc gaa atg Ile Ser Ala Leu His Arg Asn Ser Lys Pro Val Glu Val Val Glu Met 625	630	635	1920
gcg aat atg ggt agc atc gct cgc gct taa Ala Asn Met Gly Ser Ile Ala Arg Ala 645			1950

<210> SEQ ID NO 8

<211> LENGTH: 649

<212> TYPE: PRT

<213> ORGANISM: Zymomonas mobilis

<400> SEQUENCE: 8

Met Phe Pro Asn Asp Lys Thr Pro Leu Leu Asp Lys Ile Lys Thr Pro
1 5 10 15Ala Glu Leu Arg Gln Leu Asp Arg Asn Ser Leu Arg Gln Leu Ala Asp
20 25 30Glu Leu Arg Lys Glu Thr Ile Ser Ala Val Gly Val Thr Gly Gly His
35 40 45

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Leu Gly Ser Gly Leu Gly Val Ile Glu Leu Thr Val Ala Leu His Tyr
 50 55 60
 Val Phe Asn Thr Pro Lys Asp Ala Leu Val Trp Asp Val Gly His Gln
 65 70 75 80
 Thr Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Asp Arg Ile Arg Thr
 85 90 95
 Leu Arg Gln Arg Asp Gly Leu Ser Gly Phe Thr Gln Arg Ala Glu Ser
 100 105 110
 Glu Tyr Asp Ala Phe Gly Ala Ala His Ser Ser Thr Ser Ile Ser Ala
 115 120 125
 Ala Leu Gly Phe Ala Met Ala Ser Lys Leu Ser Asp Ser Asp Asp Lys
 130 135 140
 Ala Val Ala Ile Ile Gly Asp Gly Ser Met Thr Ala Gly Met Ala Tyr
 145 150 155 160
 Glu Ala Met Asn Asn Ala Lys Ala Ala Gly Lys Arg Leu Ile Val Ile
 165 170 175
 Leu Asn Asp Asn Glu Met Ser Ile Ser Pro Pro Val Gly Ala Leu Ser
 180 185 190
 Ser Tyr Leu Ser Arg Leu Ile Ser Ser Arg Pro Phe Met Asn Leu Arg
 195 200 205
 Asp Ile Met Arg Gly Val Val Asn Arg Met Pro Lys Gly Leu Ala Thr
 210 215 220
 Ala Ala Arg Lys Ala Asp Glu Tyr Ala Arg Gly Met Ala Thr Gly Gly
 225 230 235 240
 Thr Phe Phe Glu Glu Leu Gly Phe Tyr Tyr Val Gly Pro Val Asp Gly
 245 250 255
 His Asn Leu Asp Gln Leu Ile Pro Val Leu Glu Asn Val Arg Asp Ala
 260 265 270
 Lys Asp Gly Pro Ile Leu Val His Val Val Thr Arg Lys Gly Gln Gly
 275 280 285
 Tyr Ala Pro Ala Glu Ala Ala Lys Asp Lys Tyr His Ala Val Gln Arg
 290 295 300
 Leu Asp Val Val Ser Gly Lys Gln Ala Lys Ala Pro Pro Gly Pro Pro
 305 310 315 320
 Ser Tyr Thr Ser Val Phe Ser Glu Gln Leu Ile Lys Glu Ala Lys Gln
 325 330 335
 Asp Asp Lys Ile Val Thr Ile Thr Ala Ala Met Pro Thr Gly Thr Gly
 340 345 350
 Leu Asp Arg Phe Gln Gln Tyr Phe Pro Glu Arg Met Phe Asp Val Gly
 355 360 365
 Ile Ala Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu Ala Ala Ala
 370 375 380
 Gly Tyr Lys Pro Phe Cys Cys Leu Tyr Ser Thr Phe Leu Gln Arg Gly
 385 390 395 400
 Tyr Asp Gln Leu Val His Asp Val Ala Ile Gln Asn Leu Pro Val Arg
 405 410 415
 Phe Ala Val Asp Arg Ala Gly Leu Val Gly Ala Asp Gly Ala Thr His
 420 425 430
 Ala Gly Ser Phe Asp Leu Ala Phe Met Val Asn Leu Pro Asn Met Val
 435 440 445
 Val Met Ala Pro Ser Asp Glu Arg Glu Leu Ala Asn Met Val His Ser
 450 455 460
 Met Ala His Tyr Asp Gln Gly Pro Ile Ser Val Arg Tyr Pro Arg Gly

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465		470		475		480
Asn Gly Val Gly Val Ser Leu Glu Gly Glu Lys Glu Ile Leu Pro Ile		485		490		495
Gly Lys Gly Arg Leu Ile Arg Arg Gly Lys Lys Val Ala Ile Leu Ser		500		505		510
Leu Gly Thr Arg Leu Glu Glu Ser Leu Lys Ala Ala Asp Arg Leu Asp		515		520		525
Ala Gln Gly Leu Ser Thr Ser Val Ala Asp Met Arg Phe Ala Lys Pro		530		535		540
Leu Asp Glu Ala Leu Thr Arg Gln Leu Leu Lys Ser His Gln Val Ile		545		550		555
Ile Thr Ile Glu Glu Gly Ala Leu Gly Gly Phe Ala Thr Gln Val Leu		565		570		575
Thr Met Ala Ser Asp Glu Gly Leu Met Asp Asp Gly Leu Lys Ile Arg		580		585		590
Thr Leu Arg Leu Pro Asp Arg Phe Gln Pro Gln Asp Lys Gln Glu Arg		595		600		605
Gln Tyr Ala Glu Ala Gly Leu Asp Ala Asp Gly Ile Val Ala Ala Val		610		615		620
Ile Ser Ala Leu His Arg Asn Ser Lys Pro Val Glu Val Val Glu Met		625		630		635
Ala Asn Met Gly Ser Ile Ala Arg Ala		645				

<210> SEQ ID NO 9
 <211> LENGTH: 1170
 <212> TYPE: DNA
 <213> ORGANISM: Zymomonas mobilis
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(1170)

<400> SEQUENCE: 9

ttg aaa cga aaa att gct cca ata tct gtt ttt gcc gga tca gtc ttg	48
Leu Lys Arg Lys Ile Ala Pro Ile Ser Val Phe Ala Gly Ser Val Leu	
1 5 10 15	
atg atg ctg acg gcc tgt cac cat caa tcc caa gaa gcc gaa ccg gca	96
Met Met Leu Thr Ala Cys His His Gln Ser Gln Glu Ala Glu Pro Ala	
20 25 30	
ttg caa gat gtt agt ttt gtt acc gta aaa acg cag cct ttg acc gtt	144
Leu Gln Asp Val Ser Phe Val Thr Val Lys Thr Gln Pro Leu Thr Val	
35 40 45	
cat agc acc tta ccc ggt cgc act tcg gct tat gag gtg gcg gaa gta	192
His Ser Thr Leu Pro Gly Arg Thr Ser Ala Tyr Glu Val Ala Glu Val	
50 55 60	
aga cct cag gta aat ggg gtc gtt ttg gcg cgc tat ttt aac gaa ggc	240
Arg Pro Gln Val Asn Gly Val Val Leu Ala Arg Tyr Phe Asn Glu Gly	
65 70 75 80	
acg gat gtc aaa aaa ggg cag ccg cta ttc ctt atc aat ccg gct cct	288
Thr Asp Val Lys Lys Gly Gln Pro Leu Phe Leu Ile Asn Pro Ala Pro	
85 90 95	
tat caa gcg act tat gac gtt aat aaa gcg caa tta gct cat gct gaa	336
Tyr Gln Ala Thr Tyr Asp Val Asn Lys Ala Gln Leu Ala His Ala Glu	
100 105 110	
gcg caa gag aaa acg gct gct gct aaa tta gaa cgc tat aag gct ttg	384
Ala Gln Glu Lys Thr Ala Ala Ala Lys Leu Glu Arg Tyr Lys Ala Leu	
115 120 125	
gct ccg gcg cag gcg att agt cgt cag gat tat gat gat gct ttg gcc	432

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Ala	Pro	Ala	Gln	Ala	Ile	Ser	Arg	Gln	Asp	Tyr	Asp	Asp	Ala	Leu	Ala		
	130					135					140						
acc	gat	cgc	gcg	gcc	aag	gca	gat	att	gcc	caa	gcc	aaa	gcg	aat	att		480
Thr	Asp	Arg	Ala	Ala	Lys	Ala	Asp	Ile	Ala	Gln	Ala	Lys	Ala	Asn	Ile		
145					150				155					160			
gaa	tta	tcg	gct	gtt	aat	ttg	gga	tac	acc	cgt	gtg	acc	gcg	cct	att		528
Glu	Leu	Ser	Ala	Val	Asn	Leu	Gly	Tyr	Thr	Arg	Val	Thr	Ala	Pro	Ile		
				165					170					175			
act	ggc	cgg	atc	ggg	cgc	ggt	ttg	aca	acg	gtc	ggt	gcc	ttg	gta	acg		576
Thr	Gly	Arg	Ile	Gly	Arg	Val	Leu	Thr	Thr	Val	Gly	Ala	Leu	Val	Thr		
			180					185					190				
tcg	ggg	caa	agt	tcg	aat	atg	gcg	att	gtg	acc	cgc	ctt	gac	ccg	att		624
Ser	Gly	Gln	Ser	Ser	Asn	Met	Ala	Ile	Val	Thr	Arg	Leu	Asp	Pro	Ile		
		195				200						205					
tat	gtc	gat	gtg	aat	ttg	cca	aca	gtc	gat	ttt	tta	cgg	ttg	cgg	cgc		672
Tyr	Val	Asp	Val	Asn	Leu	Pro	Thr	Val	Asp	Phe	Leu	Arg	Leu	Arg	Arg		
	210					215					220						
gag	tta	aaa	gcg	gga	act	ttg	aaa	cgg	aac	ggc	aat	gat	gcc	gaa	gtc		720
Glu	Leu	Lys	Ala	Gly	Thr	Leu	Lys	Arg	Asn	Gly	Asn	Asp	Ala	Glu	Val		
225					230					235				240			
tcc	ctt	att	ctc	gat	gat	aat	tcg	acc	tat	aat	caa	aaa	gga	cgg	ctg		768
Ser	Leu	Ile	Leu	Asp	Asp	Asn	Ser	Thr	Tyr	Asn	Gln	Lys	Gly	Arg	Leu		
			245						250					255			
gct	tta	agc	gaa	gtc	agt	gcc	gac	acc	cag	aca	tcg	acc	att	gtt	gtt		816
Ala	Leu	Ser	Glu	Val	Ser	Ala	Asp	Thr	Gln	Thr	Ser	Thr	Ile	Val	Val		
			260					265					270				
cgt	gcg	ggt	ttc	cca	aat	cct	gaa	cat	ttg	ttg	ctg	ccc	gga	atg	ttt		864
Arg	Ala	Val	Phe	Pro	Asn	Pro	Glu	His	Leu	Leu	Leu	Pro	Gly	Met	Phe		
		275				280						285					
gtt	tat	ggt	cgg	ata	gaa	gag	ggc	ggt	gat	ccg	aac	gcc	ttg	ttg	gtt		912
Val	Tyr	Gly	Arg	Ile	Glu	Glu	Gly	Val	Asp	Pro	Asn	Ala	Leu	Leu	Val		
	290					295					300						
ccg	caa	gaa	tcc	gtt	ttc	cga	aat	aac	cac	ggt	gat	ccg	atg	tta	tat		960
Pro	Gln	Glu	Ser	Val	Phe	Arg	Asn	Asn	His	Gly	Asp	Pro	Met	Leu	Tyr		
305					310					315				320			
gtc	gtc	aat	aaa	gac	gac	ggt	att	gaa	gca	cgc	ccg	ata	aaa	acc	ggt		1008
Val	Val	Asn	Lys	Asp	Asp	Val	Ile	Glu	Ala	Arg	Pro	Ile	Lys	Thr	Gly		
				325					330					335			
gaa	gct	atc	gga	acg	caa	tgg	gct	gtg	aca	tcc	ggt	ttg	caa	aaa	ggc		1056
Glu	Ala	Ile	Gly	Thr	Gln	Trp	Ala	Val	Thr	Ser	Gly	Leu	Gln	Lys	Gly		
			340					345					350				
gaa	cgc	ggt	ttg	gtc	tct	ggt	ctt	caa	aaa	gtg	aat	atc	ggc	gac	aaa		1104
Glu	Arg	Val	Leu	Val	Ser	Gly	Leu	Gln	Lys	Val	Asn	Ile	Gly	Asp	Lys		
		355					360					365					
gtt	cat	ccg	aca	gag	gct	tct	ctt	acc	aaa	gat	gcc	tcg	cca	gaa	aag		1152
Val	His	Pro	Thr	Glu	Ala	Ser	Leu	Thr	Lys	Asp	Ala	Ser	Pro	Glu	Lys		
	370					375					380						
aag	ggc	ggc	aag	gcg	taa												1170
Lys	Gly	Gly	Lys	Ala													
385																	

<210> SEQ ID NO 10

<211> LENGTH: 389

<212> TYPE: PRT

<213> ORGANISM: Zymomonas mobilis

<400> SEQUENCE: 10

Leu Lys Arg Lys Ile Ala Pro Ile Ser Val Phe Ala Gly Ser Val Leu
 1 5 10 15

Met Met Leu Thr Ala Cys His His Gln Ser Gln Glu Ala Glu Pro Ala

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20					25					30					
Leu	Gln	Asp	Val	Ser	Phe	Val	Thr	Val	Lys	Thr	Gln	Pro	Leu	Thr	Val
		35					40					45			
His	Ser	Thr	Leu	Pro	Gly	Arg	Thr	Ser	Ala	Tyr	Glu	Val	Ala	Glu	Val
	50					55					60				
Arg	Pro	Gln	Val	Asn	Gly	Val	Val	Leu	Ala	Arg	Tyr	Phe	Asn	Glu	Gly
65					70					75				80	
Thr	Asp	Val	Lys	Lys	Gly	Gln	Pro	Leu	Phe	Leu	Ile	Asn	Pro	Ala	Pro
				85					90					95	
Tyr	Gln	Ala	Thr	Tyr	Asp	Val	Asn	Lys	Ala	Gln	Leu	Ala	His	Ala	Glu
			100					105					110		
Ala	Gln	Glu	Lys	Thr	Ala	Ala	Ala	Lys	Leu	Glu	Arg	Tyr	Lys	Ala	Leu
		115					120					125			
Ala	Pro	Ala	Gln	Ala	Ile	Ser	Arg	Gln	Asp	Tyr	Asp	Asp	Ala	Leu	Ala
	130					135					140				
Thr	Asp	Arg	Ala	Ala	Lys	Ala	Asp	Ile	Ala	Gln	Ala	Lys	Ala	Asn	Ile
145					150					155				160	
Glu	Leu	Ser	Ala	Val	Asn	Leu	Gly	Tyr	Thr	Arg	Val	Thr	Ala	Pro	Ile
				165					170					175	
Thr	Gly	Arg	Ile	Gly	Arg	Val	Leu	Thr	Thr	Val	Gly	Ala	Leu	Val	Thr
			180					185					190		
Ser	Gly	Gln	Ser	Ser	Asn	Met	Ala	Ile	Val	Thr	Arg	Leu	Asp	Pro	Ile
		195					200					205			
Tyr	Val	Asp	Val	Asn	Leu	Pro	Thr	Val	Asp	Phe	Leu	Arg	Leu	Arg	Arg
	210					215					220				
Glu	Leu	Lys	Ala	Gly	Thr	Leu	Lys	Arg	Asn	Gly	Asn	Asp	Ala	Glu	Val
225					230					235				240	
Ser	Leu	Ile	Leu	Asp	Asp	Asn	Ser	Thr	Tyr	Asn	Gln	Lys	Gly	Arg	Leu
				245					250					255	
Ala	Leu	Ser	Glu	Val	Ser	Ala	Asp	Thr	Gln	Thr	Ser	Thr	Ile	Val	Val
			260					265					270		
Arg	Ala	Val	Phe	Pro	Asn	Pro	Glu	His	Leu	Leu	Leu	Pro	Gly	Met	Phe
		275					280						285		
Val	Tyr	Gly	Arg	Ile	Glu	Glu	Gly	Val	Asp	Pro	Asn	Ala	Leu	Leu	Val
	290					295					300				
Pro	Gln	Glu	Ser	Val	Phe	Arg	Asn	Asn	His	Gly	Asp	Pro	Met	Leu	Tyr
305					310					315				320	
Val	Val	Asn	Lys	Asp	Asp	Val	Ile	Glu	Ala	Arg	Pro	Ile	Lys	Thr	Gly
				325					330					335	
Glu	Ala	Ile	Gly	Thr	Gln	Trp	Ala	Val	Thr	Ser	Gly	Leu	Gln	Lys	Gly
			340					345					350		
Glu	Arg	Val	Leu	Val	Ser	Gly	Leu	Gln	Lys	Val	Asn	Ile	Gly	Asp	Lys
		355					360					365			
Val	His	Pro	Thr	Glu	Ala	Ser	Leu	Thr	Lys	Asp	Ala	Ser	Pro	Glu	Lys
	370					375					380				
Lys	Gly	Gly	Lys	Ala											
385															

<210> SEQ ID NO 11

<211> LENGTH: 3144

<212> TYPE: DNA

<213> ORGANISM: Zymomonas mobilis

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(3144)

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<400> SEQUENCE: 11

atg gct cgc tat ttt att gac cgc cct gtt ttt gct tgg gtt atc ggt	48
Met Ala Arg Tyr Phe Ile Asp Arg Pro Val Phe Ala Trp Val Ile Gly	
1 5 10 15	
ctt atc atc atg tta ttg ggt gcc ttg gca att gtt aaa atg cct att	96
Leu Ile Ile Met Leu Leu Gly Ala Leu Ala Ile Val Lys Met Pro Ile	
20 25 30	
gcc caa tat ccg aat gtt gcc cct ccg cag att gag atc agt gtg tct	144
Ala Gln Tyr Pro Asn Val Ala Pro Pro Gln Ile Glu Ile Ser Val Ser	
35 40 45	
tat ccg ggg gcg tcg gct gaa acg atc aat aat acc gtt gtt cgg cct	192
Tyr Pro Gly Ala Ser Ala Glu Thr Ile Asn Asn Thr Val Val Arg Pro	
50 55 60	
atc tta cag cag atg cat ggc atc gat aat ctg gaa tat att tcg gct	240
Ile Leu Gln Gln Met His Gly Ile Asp Asn Leu Glu Tyr Ile Ser Ala	
65 70 75 80	
tct tcc ttt gca tca ggt cag atg acg att gat ttg acc ttt gca caa	288
Ser Ser Phe Ala Ser Gly Gln Met Thr Ile Asp Leu Thr Phe Ala Gln	
85 90 95	
ggt acc gat gcc gat atc gca cag gtg caa gtc cag aat aaa tta caa	336
Gly Thr Asp Ala Asp Ile Ala Gln Val Gln Val Gln Asn Lys Leu Gln	
100 105 110	
tta gcg cag cct cgt ttg ccg tcg gat gtg gtc aat cag ggt att acg	384
Leu Ala Gln Pro Arg Leu Pro Ser Asp Val Val Asn Gln Gly Ile Thr	
115 120 125	
gtt aac cgt tct gcc aaa agt ttt atg atg att atg tcc ttc atc tcg	432
Val Asn Arg Ser Ala Lys Ser Phe Met Met Ile Met Ser Phe Ile Ser	
130 135 140	
acc gat ggc agt atg tcc tat cag gac atc aac gat tat gtg gca tcg	480
Thr Asp Gly Ser Met Ser Tyr Gln Asp Ile Asn Asp Tyr Val Ala Ser	
145 150 155 160	
aat att gct gat ccg ttg agc cgt gtt tcc ggt gtc ggc gat tac act	528
Asn Ile Ala Asp Pro Leu Ser Arg Val Ser Gly Val Gly Asp Tyr Thr	
165 170 175	
ctg ttc ggt ttt gaa tat gca atg cgg gtc tgg tta gat cca gca aag	576
Leu Phe Gly Phe Glu Tyr Ala Met Arg Val Trp Leu Asp Pro Ala Lys	
180 185 190	
ctc tac aaa tat aat ttg act gta gcg gat gtc caa tca gct att tct	624
Leu Tyr Lys Tyr Asn Leu Thr Val Ala Asp Val Gln Ser Ala Ile Ser	
195 200 205	
acc cag aat att cag ctt tca tcc ggt gaa ttg ggc gga ttg cct gcg	672
Thr Gln Asn Ile Gln Leu Ser Ser Gly Glu Leu Gly Gly Leu Pro Ala	
210 215 220	
gtt cag ggt att cgt ttg gat gcg acc att att ggc ccg acc cgt ttg	720
Val Gln Gly Ile Arg Leu Asp Ala Thr Ile Ile Gly Pro Thr Arg Leu	
225 230 235 240	
acc tcg cct gaa gaa ttt aaa aat att ctg gtc aag gct ttg ccg gat	768
Thr Ser Pro Glu Glu Phe Lys Asn Ile Leu Val Lys Ala Leu Pro Asp	
245 250 255	
ggc gcc caa atc aaa ttg ggt gac atc gct aaa gta gag ttg ggc gcg	816
Gly Ala Gln Ile Lys Leu Gly Asp Ile Ala Lys Val Glu Leu Gly Ala	
260 265 270	
caa agc tat aac ttt gac gtg cgc tat aat aac cag ccg gct tcg ggt	864
Gln Ser Tyr Asn Phe Asp Val Arg Tyr Asn Asn Gln Pro Ala Ser Gly	
275 280 285	
att gcg atc aaa ttg gca ccg ggg gcg aac cag ctt caa act gaa aag	912
Ile Ala Ile Lys Leu Ala Pro Gly Ala Asn Gln Leu Gln Thr Glu Lys	
290 295 300	

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ttg atc cgt cag cgt ttg gcc gat ttg gaa cct ttc ttc cct cat ggt	960
Leu Ile Arg Gln Arg Leu Ala Asp Leu Glu Pro Phe Phe Pro His Gly	
305 310 315 320	
ttg aag gtc gaa tat ccg gtt gat acc aag cca ttt gtg acg gct tct	1008
Leu Lys Val Glu Tyr Pro Val Asp Thr Lys Pro Phe Val Thr Ala Ser	
325 330 335	
atc cat gag gtt att gaa acc ttg gtg gaa gct att gcg ctt gtt ttc	1056
Ile His Glu Val Ile Glu Thr Leu Val Glu Ala Ile Ala Leu Val Phe	
340 345 350	
ttg gtg atg ctg atc ttc ttg cag aat ttc cgt gct acc ttg atc ccg	1104
Leu Val Met Leu Ile Phe Leu Gln Asn Phe Arg Ala Thr Leu Ile Pro	
355 360 365	
acg att gct gtg cca gtg gtg ttg tta ggc acc ttt ggt gtg ctt tct	1152
Thr Ile Ala Val Pro Val Val Leu Leu Gly Thr Phe Gly Val Leu Ser	
370 375 380	
gtt ctt ggt ttt tca atc aat act ctg acg atg ttg gca atg gtc ttg	1200
Val Leu Gly Phe Ser Ile Asn Thr Leu Thr Met Leu Ala Met Val Leu	
385 390 395 400	
gct gtt ggc ttg ttg gtc gat gat gcc atc gtc gtt gtt gaa aat gtc	1248
Ala Val Gly Leu Leu Val Asp Asp Ala Ile Val Val Val Glu Asn Val	
405 410 415	
gaa cgt ttg atg cga gat gaa aag ctg ccc ccg aaa gag gcg gcg aag	1296
Glu Arg Leu Met Arg Asp Glu Lys Leu Pro Pro Lys Glu Ala Ala Lys	
420 425 430	
cgc tcg atg gat gaa att tct ggt gct ttg atc ggt atc gtc ttg gtc	1344
Arg Ser Met Asp Glu Ile Ser Gly Ala Leu Ile Gly Ile Val Leu Val	
435 440 445	
ttg tcg gcc gtg ttc ttg cct atg gcg gcc ttt tca ggg tca acg ggc	1392
Leu Ser Ala Val Phe Leu Pro Met Ala Ala Phe Ser Gly Ser Thr Gly	
450 455 460	
gtt atc tat cgc caa ttc tcg att acg att gtg gtg gcg atg ggg ctg	1440
Val Ile Tyr Arg Gln Phe Ser Ile Thr Ile Val Val Ala Met Gly Leu	
465 470 475 480	
tct gtc ctt gtg gcg atg att atg acg cca gcc ctt tgc gca acg atg	1488
Ser Val Leu Val Ala Met Ile Met Thr Pro Ala Leu Cys Ala Thr Met	
485 490 495	
tta aag ccg att gac cat gac caa gcc gat aaa aag ccg ggt atc ttt	1536
Leu Lys Pro Ile Asp His Asp Gln Ala Asp Lys Lys Pro Gly Ile Phe	
500 505 510	
ggt cgc ttg gcg aat ggc ttt aac cgt gct ttt gac cga ttg aat aat	1584
Gly Arg Leu Ala Asn Gly Phe Asn Arg Ala Phe Asp Arg Leu Asn Asn	
515 520 525	
ggt tat ttg ggt ggt gtg tot tgg ttg tta gga cgt tcc gtc aaa ggc	1632
Gly Tyr Leu Gly Gly Val Ser Trp Leu Leu Gly Arg Ser Val Lys Gly	
530 535 540	
ggc att gcc ttt ttg atc att gtt ttc gcc gtt ggt tat tta ttc act	1680
Gly Ile Ala Phe Leu Ile Ile Val Phe Ala Val Gly Tyr Leu Phe Thr	
545 550 555 560	
cgc ttg cca acc gga ttt ttg ccg gat gaa gat cag ggt gaa ttt att	1728
Arg Leu Pro Thr Gly Phe Leu Pro Asp Glu Asp Gln Gly Glu Phe Ile	
565 570 575	
ggt cag gtg acc tta ccg ccg ggg gcg acc caa gaa caa acg tcg gaa	1776
Gly Gln Val Thr Leu Pro Pro Gly Ala Thr Gln Glu Gln Thr Ser Glu	
580 585 590	
gcg gtg cgc aag gtt aat gat tat ctt ctg tcc gca gag aaa gac agt	1824
Ala Val Arg Lys Val Asn Asp Tyr Leu Leu Ser Ala Glu Lys Asp Ser	
595 600 605	
gtc ata tct gtg atg acg gtt agc ggt ttt aac ttt ggt ggt cag gga	1872
Val Ile Ser Val Met Thr Val Ser Gly Phe Asn Phe Gly Gly Gln Gly	
610 615 620	

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caa aat gcc ggt tct ttc ttc gtt cgt ttg aaa cct tgg gat cag cgt Gln Asn Ala Gly Ser Phe Phe Val Arg Leu Lys Pro Trp Asp Gln Arg 625 630 635 640	1920
ccg aaa gcc tcg caa agt gct tcg gcc ttg gca atg cgg acg atg atg Pro Lys Ala Ser Gln Ser Ala Ser Ala Leu Ala Met Arg Thr Met Met 645 650 655	1968
cat ttt tgg ggt gat ccg tca tcg atg act ttt gcc ttt aat atg cct His Phe Trp Gly Asp Pro Ser Ser Met Thr Phe Ala Phe Asn Met Pro 660 665 670	2016
gct gtc cgc gac ttg ggt aat gcc acc ggt ttt gac ctt gaa ctg gaa Ala Val Arg Asp Leu Gly Asn Ala Thr Gly Phe Asp Leu Glu Leu Glu 675 680 685	2064
gat cgc ggt cat atc ggt cat gca aaa ttc ctt gaa gcc cgt aac atg Asp Arg Gly His Ile Gly His Ala Lys Phe Leu Glu Ala Arg Asn Met 690 695 700	2112
tta ttg gct ttg gcc tcg aaa gat ccc cgc tta agt ggt gtc cgt ccg Leu Leu Ala Leu Ala Ser Lys Asp Pro Arg Leu Ser Gly Val Arg Pro 705 710 715 720	2160
aat ggt atg gaa gat gcc cct caa tat cat ttg acc gtt gat tac ggc Asn Gly Met Glu Asp Ala Pro Gln Tyr His Leu Thr Val Asp Tyr Gly 725 730 735	2208
aaa gct gtt atg atg gga ttg acc cca aat gat gtg aat gtg gcc ttg Lys Ala Val Met Met Gly Leu Thr Pro Asn Asp Val Asn Val Ala Leu 740 745 750	2256
cag ggg tct ttg ggg tcg att tac gtc aat cag ttt atg cgg gat gac Gln Gly Ser Leu Gly Ser Ile Tyr Val Asn Gln Phe Met Arg Asp Asp 755 760 765	2304
cgt gtg aag cag gtc tat tta atg ggg gca ccg gaa gcg cgt atg ctg Arg Val Lys Gln Val Tyr Leu Met Gly Ala Pro Glu Ala Arg Met Leu 770 775 780	2352
cct tcc gat ttt tcc aaa tgg tat ctg cgg aat aat gtc ggc acg atg Pro Ser Asp Phe Ser Lys Trp Tyr Leu Arg Asn Asn Val Gly Thr Met 785 790 795 800	2400
gtt ccc ttt agc gcc ttt atg aca gga aca tgg caa acg ggc cct cag Val Pro Phe Ser Ala Phe Met Thr Gly Thr Trp Gln Thr Gly Pro Gln 805 810 815	2448
aaa gtc gaa aat tat aac ggc tat aat tct ttc gaa att atg ggc gcg Lys Val Glu Asn Tyr Asn Gly Tyr Asn Ser Phe Glu Ile Met Gly Ala 820 825 830	2496
cct gca ccg gga cat agt tcg ggt gaa gcc att cag gcg atg acc gag Pro Ala Pro Gly His Ser Ser Gly Glu Ala Ile Gln Ala Met Thr Glu 835 840 845	2544
atc gtt cat aaa ttg cca gct ggt gtt ggg cat gaa tgg aca ggg tta Ile Val His Lys Leu Pro Ala Gly Val Gly His Glu Trp Thr Gly Leu 850 855 860	2592
tct ttt gaa gag cag gcg gcc ggt tcg tcc acc atg tct ctt tat gcg Ser Phe Glu Glu Gln Ala Ala Gly Ser Ser Thr Met Ser Leu Tyr Ala 865 870 875 880	2640
att tcc gcg att gtg gtt ctg ttc tgt ctt gcc gca ctt tat gaa agc Ile Ser Ala Ile Val Val Leu Phe Cys Leu Ala Ala Leu Tyr Glu Ser 885 890 895	2688
tgg gcc gtg ccg tta tcg gtt att ttg gtt ctg cct ttg ggt gtc ttg Trp Ala Val Pro Leu Ser Val Ile Leu Val Leu Pro Leu Gly Val Leu 900 905 910	2736
ggt gcc gtt gta gca acc ttg atg cgt gga ttg tcg aat gac gtc tat Gly Ala Val Val Ala Thr Leu Met Arg Gly Leu Ser Asn Asp Val Tyr 915 920 925	2784
ttc cag atc ggt ttg ctg acg acc gtt ggt ttg acc gtt aaa aac gct Phe Gln Ile Gly Leu Leu Thr Thr Val Gly Leu Thr Val Lys Asn Ala	2832

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930	935	940	
att ttg att gtc gaa ttt gca aaa gcc ttt ttc gat aat gcc gtg cca			2880
Ile Leu Ile Val Glu Phe Ala Lys Ala Phe Phe Asp Asn Gly Val Pro			
945	950	955	960
ctt ttg caa tcg gtg gtt caa gca ggc cgt gag cgg tta cgg cct att			2928
Leu Leu Gln Ser Val Val Gln Ala Gly Arg Glu Arg Leu Arg Pro Ile			
	965	970	975
ttg atg acc tct att gct ttt gtg ttg ggg gtt att cca ttg agc atc			2976
Leu Met Thr Ser Ile Ala Phe Val Leu Gly Val Ile Pro Leu Ser Ile			
	980	985	990
gca aca ggg gct tct tcg gca gca cgt atc gct atc gga acg gcc gtt			3024
Ala Thr Gly Ala Ser Ser Ala Ala Arg Ile Ala Ile Gly Thr Ala Val			
	995	1000	1005
gtc ggc ggg atg gtg acg gct acc ttg ttg acg att ttc ttt gtg			3069
Val Gly Gly Met Val Thr Ala Thr Leu Leu Thr Ile Phe Phe Val			
	1010	1015	1020
cct ctt ttc ttt gtg gtg gtt ttg aag ctg ttt cgg gtg aaa ccg			3114
Pro Leu Phe Phe Val Val Val Leu Lys Leu Phe Arg Val Lys Pro			
	1025	1030	1035
aac aag ctg aat gcg gag gaa gca gcc tga			3144
Asn Lys Leu Asn Ala Glu Glu Ala Ala			
	1040	1045	

<210> SEQ ID NO 12

<211> LENGTH: 1047

<212> TYPE: PRT

<213> ORGANISM: Zymomonas mobilis

<400> SEQUENCE: 12

Met Ala Arg Tyr Phe Ile Asp Arg Pro Val Phe Ala Trp Val Ile Gly			
1	5	10	15
Leu Ile Ile Met Leu Leu Gly Ala Leu Ala Ile Val Lys Met Pro Ile			
	20	25	30
Ala Gln Tyr Pro Asn Val Ala Pro Pro Gln Ile Glu Ile Ser Val Ser			
	35	40	45
Tyr Pro Gly Ala Ser Ala Glu Thr Ile Asn Asn Thr Val Val Arg Pro			
	50	55	60
Ile Leu Gln Gln Met His Gly Ile Asp Asn Leu Glu Tyr Ile Ser Ala			
	65	70	75
Ser Ser Phe Ala Ser Gly Gln Met Thr Ile Asp Leu Thr Phe Ala Gln			
	85	90	95
Gly Thr Asp Ala Asp Ile Ala Gln Val Gln Val Gln Asn Lys Leu Gln			
	100	105	110
Leu Ala Gln Pro Arg Leu Pro Ser Asp Val Val Asn Gln Gly Ile Thr			
	115	120	125
Val Asn Arg Ser Ala Lys Ser Phe Met Met Ile Met Ser Phe Ile Ser			
	130	135	140
Thr Asp Gly Ser Met Ser Tyr Gln Asp Ile Asn Asp Tyr Val Ala Ser			
	145	150	155
Asn Ile Ala Asp Pro Leu Ser Arg Val Ser Gly Val Gly Asp Tyr Thr			
	165	170	175
Leu Phe Gly Phe Glu Tyr Ala Met Arg Val Trp Leu Asp Pro Ala Lys			
	180	185	190
Leu Tyr Lys Tyr Asn Leu Thr Val Ala Asp Val Gln Ser Ala Ile Ser			
	195	200	205
Thr Gln Asn Ile Gln Leu Ser Ser Gly Glu Leu Gly Gly Leu Pro Ala			
	210	215	220

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Val Gln Gly Ile Arg Leu Asp Ala Thr Ile Ile Gly Pro Thr Arg Leu
 225 230 235 240
 Thr Ser Pro Glu Glu Phe Lys Asn Ile Leu Val Lys Ala Leu Pro Asp
 245 250 255
 Gly Ala Gln Ile Lys Leu Gly Asp Ile Ala Lys Val Glu Leu Gly Ala
 260 265 270
 Gln Ser Tyr Asn Phe Asp Val Arg Tyr Asn Asn Gln Pro Ala Ser Gly
 275 280 285
 Ile Ala Ile Lys Leu Ala Pro Gly Ala Asn Gln Leu Gln Thr Glu Lys
 290 295 300
 Leu Ile Arg Gln Arg Leu Ala Asp Leu Glu Pro Phe Phe Pro His Gly
 305 310 315 320
 Leu Lys Val Glu Tyr Pro Val Asp Thr Lys Pro Phe Val Thr Ala Ser
 325 330 335
 Ile His Glu Val Ile Glu Thr Leu Val Glu Ala Ile Ala Leu Val Phe
 340 345 350
 Leu Val Met Leu Ile Phe Leu Gln Asn Phe Arg Ala Thr Leu Ile Pro
 355 360 365
 Thr Ile Ala Val Pro Val Val Leu Leu Gly Thr Phe Gly Val Leu Ser
 370 375 380
 Val Leu Gly Phe Ser Ile Asn Thr Leu Thr Met Leu Ala Met Val Leu
 385 390 395 400
 Ala Val Gly Leu Leu Val Asp Asp Ala Ile Val Val Val Glu Asn Val
 405 410 415
 Glu Arg Leu Met Arg Asp Glu Lys Leu Pro Pro Lys Glu Ala Ala Lys
 420 425 430
 Arg Ser Met Asp Glu Ile Ser Gly Ala Leu Ile Gly Ile Val Leu Val
 435 440 445
 Leu Ser Ala Val Phe Leu Pro Met Ala Ala Phe Ser Gly Ser Thr Gly
 450 455 460
 Val Ile Tyr Arg Gln Phe Ser Ile Thr Ile Val Val Ala Met Gly Leu
 465 470 475 480
 Ser Val Leu Val Ala Met Ile Met Thr Pro Ala Leu Cys Ala Thr Met
 485 490 495
 Leu Lys Pro Ile Asp His Asp Gln Ala Asp Lys Lys Pro Gly Ile Phe
 500 505 510
 Gly Arg Leu Ala Asn Gly Phe Asn Arg Ala Phe Asp Arg Leu Asn Asn
 515 520 525
 Gly Tyr Leu Gly Gly Val Ser Trp Leu Leu Gly Arg Ser Val Lys Gly
 530 535 540
 Gly Ile Ala Phe Leu Ile Ile Val Phe Ala Val Gly Tyr Leu Phe Thr
 545 550 555 560
 Arg Leu Pro Thr Gly Phe Leu Pro Asp Glu Asp Gln Gly Glu Phe Ile
 565 570 575
 Gly Gln Val Thr Leu Pro Pro Gly Ala Thr Gln Glu Gln Thr Ser Glu
 580 585 590
 Ala Val Arg Lys Val Asn Asp Tyr Leu Leu Ser Ala Glu Lys Asp Ser
 595 600 605
 Val Ile Ser Val Met Thr Val Ser Gly Phe Asn Phe Gly Gly Gln Gly
 610 615 620
 Gln Asn Ala Gly Ser Phe Phe Val Arg Leu Lys Pro Trp Asp Gln Arg
 625 630 635 640

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Pro	Lys	Ala	Ser	Gln	Ser	Ala	Ser	Ala	Leu	Ala	Met	Arg	Thr	Met	Met	645	650	655	
His	Phe	Trp	Gly	Asp	Pro	Ser	Ser	Met	Thr	Phe	Ala	Phe	Asn	Met	Pro	660	665	670	
Ala	Val	Arg	Asp	Leu	Gly	Asn	Ala	Thr	Gly	Phe	Asp	Leu	Glu	Leu	Glu	675	680	685	
Asp	Arg	Gly	His	Ile	Gly	His	Ala	Lys	Phe	Leu	Glu	Ala	Arg	Asn	Met	690	695	700	
Leu	Leu	Ala	Leu	Ala	Ser	Lys	Asp	Pro	Arg	Leu	Ser	Gly	Val	Arg	Pro	705	710	715	720
Asn	Gly	Met	Glu	Asp	Ala	Pro	Gln	Tyr	His	Leu	Thr	Val	Asp	Tyr	Gly	725	730	735	
Lys	Ala	Val	Met	Met	Gly	Leu	Thr	Pro	Asn	Asp	Val	Asn	Val	Ala	Leu	740	745	750	
Gln	Gly	Ser	Leu	Gly	Ser	Ile	Tyr	Val	Asn	Gln	Phe	Met	Arg	Asp	Asp	755	760	765	
Arg	Val	Lys	Gln	Val	Tyr	Leu	Met	Gly	Ala	Pro	Glu	Ala	Arg	Met	Leu	770	775	780	
Pro	Ser	Asp	Phe	Ser	Lys	Trp	Tyr	Leu	Arg	Asn	Asn	Val	Gly	Thr	Met	785	790	795	800
Val	Pro	Phe	Ser	Ala	Phe	Met	Thr	Gly	Thr	Trp	Gln	Thr	Gly	Pro	Gln	805	810	815	
Lys	Val	Glu	Asn	Tyr	Asn	Gly	Tyr	Asn	Ser	Phe	Glu	Ile	Met	Gly	Ala	820	825	830	
Pro	Ala	Pro	Gly	His	Ser	Ser	Gly	Glu	Ala	Ile	Gln	Ala	Met	Thr	Glu	835	840	845	
Ile	Val	His	Lys	Leu	Pro	Ala	Gly	Val	Gly	His	Glu	Trp	Thr	Gly	Leu	850	855	860	
Ser	Phe	Glu	Glu	Gln	Ala	Ala	Gly	Ser	Ser	Thr	Met	Ser	Leu	Tyr	Ala	865	870	875	880
Ile	Ser	Ala	Ile	Val	Val	Leu	Phe	Cys	Leu	Ala	Ala	Leu	Tyr	Glu	Ser	885	890	895	
Trp	Ala	Val	Pro	Leu	Ser	Val	Ile	Leu	Val	Leu	Pro	Leu	Gly	Val	Leu	900	905	910	
Gly	Ala	Val	Val	Ala	Thr	Leu	Met	Arg	Gly	Leu	Ser	Asn	Asp	Val	Tyr	915	920	925	
Phe	Gln	Ile	Gly	Leu	Leu	Thr	Thr	Val	Gly	Leu	Thr	Val	Lys	Asn	Ala	930	935	940	
Ile	Leu	Ile	Val	Glu	Phe	Ala	Lys	Ala	Phe	Phe	Asp	Asn	Gly	Val	Pro	945	950	955	960
Leu	Leu	Gln	Ser	Val	Val	Gln	Ala	Gly	Arg	Glu	Arg	Leu	Arg	Pro	Ile	965	970	975	
Leu	Met	Thr	Ser	Ile	Ala	Phe	Val	Leu	Gly	Val	Ile	Pro	Leu	Ser	Ile	980	985	990	
Ala	Thr	Gly	Ala	Ser	Ser	Ala	Ala	Arg	Ile	Ala	Ile	Gly	Thr	Ala	Val	995	1000	1005	
Val	Gly	Gly	Met	Val	Thr	Ala	Thr	Leu	Leu	Thr	Ile	Phe	Phe	Val	1010	1015	1020		
Pro	Leu	Phe	Phe	Val	Val	Val	Leu	Lys	Leu	Phe	Arg	Val	Lys	Pro	1025	1030	1035		
Asn	Lys	Leu	Asn	Ala	Glu	Glu	Ala	Ala	1040	1045									

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<210> SEQ ID NO 13
<211> LENGTH: 1539
<212> TYPE: DNA
<213> ORGANISM: Zymomonas mobilis
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1539)

<400> SEQUENCE: 13

atg act tta ttt tcg gct tct tcg gct ctg att aag cgg agt aaa aaa      48
Met Thr Leu Phe Ser Ala Ser Ser Ala Leu Ile Lys Arg Ser Lys Lys
1                               5                               10                               15

gga tgg cgt tat cct gta acg cta ttc tta tcg act aat att ctg ttg      96
Gly Trp Arg Tyr Pro Val Thr Leu Phe Leu Ser Thr Asn Ile Leu Leu
20                               25                               30

gct gga tgc acg atg gca ccg aaa tat cat cgt cca gca gcg tct gtg     144
Ala Gly Cys Thr Met Ala Pro Lys Tyr His Arg Pro Ala Ala Ser Val
35                               40                               45

gca ccg caa tgg ccg aaa tca gcg gca ttg cct gcc gct gat aac act     192
Ala Pro Gln Trp Pro Lys Ser Ala Ala Leu Pro Ala Ala Asp Asn Thr
50                               55                               60

tca atg aag ccc cat cct atg gca gcc gat ttg ggg tgg cag gat ttt     240
Ser Met Lys Pro His Pro Met Ala Ala Asp Leu Gly Trp Gln Asp Phe
65                               70                               75                               80

ttc aaa gat gcg cgc cta aaa gcc ctg att aca att gcg atc cgc gaa     288
Phe Lys Asp Ala Arg Leu Lys Ala Leu Ile Thr Ile Ala Ile Arg Glu
85                               90                               95

aac cgc gat ttg cgg tca gct att cag gca atc ggt gag gcg caa gcc     336
Asn Arg Asp Leu Arg Ser Ala Ile Gln Ala Ile Gly Glu Ala Gln Ala
100                              105                              110

aga tat cga gtg caa cgc gcg tct tta ttg ccc gca atc ggt ggc act     384
Arg Tyr Arg Val Gln Arg Ala Ser Leu Leu Pro Ala Ile Gly Gly Thr
115                              120                              125

ggc gaa gtg atg tat cag cag cct tcg ggt aaa tcc ggt ttg agt ttt     432
Gly Glu Val Met Tyr Gln Gln Pro Ser Gly Lys Ser Gly Leu Ser Phe
130                              135                              140

gcc cca ggt gtc ggt gaa gat att ccg cgt ttc cat tat tat tcg atg     480
Ala Pro Gly Val Gly Glu Asp Ile Pro Arg Phe His Tyr Tyr Ser Met
145                              150                              155                              160

ggt atc ggt ttt tct tct tat gaa att gat att ttt ggc cgc atc cgc     528
Gly Ile Gly Phe Ser Ser Tyr Glu Ile Asp Ile Phe Gly Arg Ile Arg
165                              170                              175

agt tta agc aag gag gcg gct gaa aga gcc ttg atg cag gaa gag act     576
Ser Leu Ser Lys Glu Ala Ala Glu Arg Ala Leu Met Gln Glu Glu Thr
180                              185                              190

gcc aga ggc acc ttg atc acg ctg att tcg cag gtg gca aat agc tat     624
Ala Arg Gly Thr Leu Ile Thr Leu Ile Ser Gln Val Ala Asn Ser Tyr
195                              200                              205

att gct tgg ttg gca gat cga gaa act ttg aat ctt gcc gaa gaa agc     672
Ile Ala Trp Leu Ala Asp Arg Glu Thr Leu Asn Leu Ala Glu Glu Ser
210                              215                              220

tat cag gct gcc aag cgg aat ttg gat ttg acg cag gct ttg ctt gac     720
Tyr Gln Ala Ala Lys Arg Asn Leu Asp Leu Thr Gln Ala Leu Leu Asp
225                              230                              235                              240

cat ggt gaa gcg agc ctt ttg acg gtc aat caa gcc gaa acc ttg ttc     768
His Gly Glu Ala Ser Leu Leu Thr Val Asn Gln Ala Glu Thr Leu Phe
245                              250                              255

cag caa aaa gca gat ttg cgg gag cag gca aag cgt cag atg gca tgg     816
Gln Gln Lys Ala Asp Leu Arg Glu Gln Ala Lys Arg Gln Met Ala Trp
260                              265                              270

gaa gaa aat aat ctt gtc ttg ctg atc ggg cag cct ttg ccc gat aat     864

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Glu	Glu	Asn	Asn	Leu	Val	Leu	Leu	Ile	Gly	Gln	Pro	Leu	Pro	Asp	Asn		
		275					280					285					
ttg	ccg	ccg	cct	ttg	ccc	ttt	ggt	gag	caa	aat	atc	atc	gaa	gat	tta	912	
Leu	Pro	Pro	Pro	Leu	Pro	Phe	Gly	Glu	Gln	Asn	Ile	Ile	Glu	Asp	Leu		
	290					295				300							
tcg	ccc	ggt	ttg	cct	tcc	gat	ctt	ttg	gaa	aac	cgg	cct	gat	att	cga	960	
Ser	Pro	Gly	Leu	Pro	Ser	Asp	Leu	Leu	Glu	Asn	Arg	Pro	Asp	Ile	Arg		
305					310					315					320		
gcc	gcg	gaa	cat	gat	tta	aag	gcc	gct	aat	gcg	gat	att	ggg	gca	gca	1008	
Ala	Ala	Glu	His	Asp	Leu	Lys	Ala	Ala	Asn	Ala	Asp	Ile	Gly	Ala	Ala		
				325					330					335			
aga	gcg	gct	ttt	ttc	cca	agg	ttg	tct	ttg	acc	tct	tcg	ggt	aac		1056	
Arg	Ala	Ala	Phe	Phe	Pro	Arg	Leu	Ser	Leu	Thr	Ser	Ser	Val	Gly	Asn		
			340					345					350				
tca	agc	ctt	aag	cct	tcc	cag	att	ttc	act	aca	gcg	gcg	aat	aca	tgg	1104	
Ser	Ser	Leu	Lys	Pro	Ser	Gln	Ile	Phe	Thr	Thr	Ala	Ala	Asn	Thr	Trp		
		355					360						365				
gga	ttc	caa	ccg	gaa	ttg	acc	gtg	cct	att	ttt	aac	tgg	ggg	caa	aat	1152	
Gly	Phe	Gln	Pro	Glu	Leu	Thr	Val	Pro	Ile	Phe	Asn	Trp	Gly	Gln	Asn		
	370					375					380						
cgc	gcc	aat	ttg	aga	att	tcc	aag	gcc	gag	cgc	gat	atg	aag	atc	acg	1200	
Arg	Ala	Asn	Leu	Arg	Ile	Ser	Lys	Ala	Glu	Arg	Asp	Met	Lys	Ile	Thr		
385					390					395					400		
gcc	tat	caa	aaa	gca	atc	caa	agt	gct	ttt	cg	gat	gtg	tcg	aat	gct	1248	
Ala	Tyr	Gln	Lys	Ala	Ile	Gln	Ser	Ala	Phe	Arg	Asp	Val	Ser	Asn	Ala		
				405					410					415			
tta	gtc	gga	cg	gat	act	tat	cg	cg	gag	gaa	gtc	gcc	ttg	act	caa	1296	
Leu	Val	Gly	Arg	Asp	Thr	Tyr	Arg	Arg	Glu	Glu	Val	Ala	Leu	Thr	Gln		
			420					425					430				
gcg	gcg	gcg	aag	gct	gaa	aat	aac	tgg	aat	tta	gcg	cg	ttg	cg	cag	1344	
Ala	Ala	Ala	Lys	Ala	Glu	Asn	Asn	Trp	Asn	Leu	Ala	Arg	Leu	Arg	Gln		
			435				440						445				
act	caa	ggc	agt	gat	tcc	gcc	atc	act	atg	ctt	aat	tac	gag	cag	act	1392	
Thr	Gln	Gly	Ser	Asp	Ser	Ala	Ile	Thr	Met	Leu	Asn	Tyr	Glu	Gln	Thr		
	450					455						460					
tat	tac	caa	gcg	gaa	tat	cag	gcg	ata	cag	aac	agg	ggt	gcg	cg	tat	1440	
Tyr	Tyr	Gln	Ala	Glu	Tyr	Gln	Ala	Ile	Gln	Asn	Arg	Val	Ala	Arg	Tyr		
465					470					475					480		
caa	aat	ttg	gtg	acg	ctc	tat	tcc	gct	ttg	ggc	ggt	ggg	gtg	aaa	gaa	1488	
Gln	Asn	Leu	Val	Thr	Leu	Tyr	Ser	Ala	Leu	Gly	Gly	Gly	Val	Lys	Glu		
				485					490					495			
aaa	gcg	gta	tct	ttg	gat	aaa	act	gat	aaa	gcc	gcc	cat	tct	gcc	cat	1536	
Lys	Ala	Val	Ser	Leu	Asp	Lys	Thr	Asp	Lys	Ala	Ala	His	Ser	Ala	His		
			500					505					510				
tga																1539	

<210> SEQ ID NO 14
 <211> LENGTH: 512
 <212> TYPE: PRT
 <213> ORGANISM: Zymomonas mobilis
 <400> SEQUENCE: 14

Met	Thr	Leu	Phe	Ser	Ala	Ser	Ser	Ala	Leu	Ile	Lys	Arg	Ser	Lys	Lys
1				5					10					15	
Gly	Trp	Arg	Tyr	Pro	Val	Thr	Leu	Phe	Leu	Ser	Thr	Asn	Ile	Leu	Leu
			20					25					30		
Ala	Gly	Cys	Thr	Met	Ala	Pro	Lys	Tyr	His	Arg	Pro	Ala	Ala	Ser	Val
		35					40					45			
Ala	Pro	Gln	Trp	Pro	Lys	Ser	Ala	Ala	Leu	Pro	Ala	Ala	Asp	Asn	Thr

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50	55	60
Ser Met Lys Pro His 65	Pro Met Ala Ala Asp 70	Leu Gly Trp Gln Asp Phe 75 80
Phe Lys Asp Ala Arg 85	Leu Lys Ala Leu Ile Thr 90	Ile Ala Ile Arg Glu 95
Asn Arg Asp Leu Arg Ser 100	Ala Ile Gln Ala Ile Gly 105	Glu Ala Gln Ala 110
Arg Tyr Arg Val Gln Arg 115	Ala Ser Leu Leu Pro Ala 120	Ile Gly Gly Thr 125
Gly Glu Val Met Tyr Gln 130	Gln Pro Ser Gly Lys Ser 135	Gly Leu Ser Phe 140
Ala Pro Gly Val Gly Glu 145	Asp Ile Pro Arg Phe His 150	Tyr Tyr Ser Met 155 160
Gly Ile Gly Phe Ser Ser 165	Tyr Glu Ile Asp Ile Phe 170	Gly Arg Ile Arg 175
Ser Leu Ser Lys Glu Ala 180	Ala Glu Arg Ala Leu Met 185	Gln Glu Glu Thr 190
Ala Arg Gly Thr Leu Ile 195	Thr Leu Ile Ser Gln Val 200	Ala Asn Ser Tyr 205
Ile Ala Trp Leu Ala Asp 210	Arg Glu Thr Leu Asn Leu 215	Ala Glu Glu Ser 220
Tyr Gln Ala Ala Lys Arg 225	Asn Leu Asp Leu Thr Gln 230	Ala Leu Leu Asp 235 240
His Gly Glu Ala Ser Leu 245	Leu Thr Val Asn Gln Ala 250	Glu Thr Leu Phe 255
Gln Gln Lys Ala Asp Leu 260	Arg Glu Gln Ala Lys Arg 265	Gln Met Ala Trp 270
Glu Glu Asn Asn Leu Val 275	Leu Leu Ile Gly Gln Pro 280	Leu Pro Asp Asn 285
Leu Pro Pro Pro Leu Pro 290	Phe Gly Glu Gln Asn Ile 295	Ile Ile Glu Asp Leu 300
Ser Pro Gly Leu Pro Ser 305	Asp Leu Leu Glu Asn Arg 310	Pro Asp Ile Arg 315 320
Ala Ala Glu His Asp Leu 325	Lys Ala Ala Asn Ala Asp 330	Ile Gly Ala Ala 335
Arg Ala Ala Phe Phe Pro 340	Arg Leu Ser Leu Thr Ser 345	Ser Val Gly Asn 350
Ser Ser Leu Lys Pro Ser 355	Gln Ile Phe Thr Thr Ala 360	Ala Asn Thr Trp 365
Gly Phe Gln Pro Glu Leu 370	Thr Val Pro Ile Phe Asn 375	Trp Gly Gln Asn 380
Arg Ala Asn Leu Arg Ile 385	Ser Lys Ala Glu Arg Asp 390	Met Lys Ile Thr 395 400
Ala Tyr Gln Lys Ala Ile 405	Gln Ser Ala Phe Arg Asp 410	Val Ser Asn Ala 415
Leu Val Gly Arg Asp Thr 420	Tyr Arg Arg Glu Glu Val 425	Ala Leu Thr Gln 430
Ala Ala Ala Lys Ala Glu 435	Asn Asn Trp Asn Leu Ala 440	Arg Leu Arg Gln 445
Thr Gln Gly Ser Asp Ser 450	Ala Ile Thr Met Leu Asn 455	Tyr Glu Gln Thr 460
Tyr Tyr Gln Ala Glu Tyr 465	Gln Ala Ile Gln Asn Arg 470	Val Ala Arg Tyr 475 480

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Gln Asn Leu Val Thr Leu Tyr Ser Ala Leu Gly Gly Gly Val Lys Glu
485 490 495

Lys Ala Val Ser Leu Asp Lys Thr Asp Lys Ala Ala His Ser Ala His
500 505 510

<210> SEQ ID NO 15

<211> LENGTH: 648

<212> TYPE: DNA

<213> ORGANISM: Zymomonas mobilis

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(648)

<400> SEQUENCE: 15

atg aca ccc gat caa tcc gat aaa agc gcc tca aaa cgc cat gta ggg 48
Met Thr Pro Asp Gln Ser Asp Lys Ser Ala Ser Lys Arg His Val Gly
1 5 10 15

cgg cct cca cag ctt gat gaa aaa aaa cgc tgt gct ctt atc tta aaa 96
Arg Pro Pro Gln Leu Asp Glu Lys Lys Arg Cys Ala Leu Ile Leu Lys
20 25 30

gcc gct gca acg gtg ctg caa acg cat gcc tat gat ggt tcc agt atg 144
Ala Ala Ala Thr Val Leu Gln Thr His Gly Tyr Asp Gly Ser Ser Met
35 40 45

gat cgg gtt gcc agt cag gca ggc atg tca aaa aag acg gtg tat caa 192
Asp Arg Val Ala Ser Gln Ala Gly Met Ser Lys Lys Thr Val Tyr Gln
50 55 60

atg ttc ccg tca aaa aag ata tta ttc acc aaa tta ctc gaa gat cgg 240
Met Phe Pro Ser Lys Lys Ile Leu Phe Thr Lys Leu Leu Glu Asp Arg
65 70 75 80

ctt ttc tcg att gaa tgg cca gaa gaa aaa atc tgc gaa gac ccc gaa 288
Leu Phe Ser Ile Glu Trp Pro Glu Glu Lys Ile Cys Glu Asp Pro Glu
85 90 95

gaa cat ctc tac tct cta ttg atc gcc att gct caa act att cta agg 336
Glu His Leu Tyr Ser Leu Leu Ile Ala Ile Ala Gln Thr Ile Leu Arg
100 105 110

ccg gat cgg gtc tgc ctg ctt cgc att tta acc gtc gaa cat aaa tca 384
Pro Asp Arg Val Cys Leu Leu Arg Ile Leu Thr Val Glu His Lys Ser
115 120 125

gaa gaa atg cgg cat att ttt agt gat att tta caa gga cat act gaa 432
Glu Glu Met Arg His Ile Phe Ser Asp Ile Leu Gln Gly His Thr Glu
130 135 140

gac aat ttg acg cgc tgg ttc tcc gaa caa caa gac aaa ggt cgc tac 480
Asp Asn Leu Thr Arg Trp Phe Ser Glu Gln Gln Asp Lys Gly Arg Tyr
145 150 155 160

cat ata tcc gac ccc ata aaa tat gcg gat atc att ttt aat atg acc 528
His Ile Ser Asp Pro Ile Lys Tyr Ala Asp Ile Ile Phe Asn Met Thr
165 170 175

gta ggc agc ctg ttg ctc gat cga ctt ttc ggt tta gaa aaa cgc cct 576
Val Gly Ser Leu Leu Asp Arg Leu Phe Gly Leu Glu Lys Arg Pro
180 185 190

gtt gaa gac aat ttt cga gat gcc att tca att ttt tta cgg ggt atc 624
Val Glu Asp Asn Phe Arg Asp Ala Ile Ser Ile Phe Leu Arg Gly Ile
195 200 205

cgt atc aat cct gaa aat gaa taa 648
Arg Ile Asn Pro Glu Asn Glu
210 215

<210> SEQ ID NO 16

<211> LENGTH: 215

<212> TYPE: PRT

<213> ORGANISM: Zymomonas mobilis

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<400> SEQUENCE: 16

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Met Thr Pro Asp Gln Ser Asp Lys Ser Ala Ser Lys Arg His Val Gly
1          5          10          15
Arg Pro Pro Gln Leu Asp Glu Lys Lys Arg Cys Ala Leu Ile Leu Lys
20          25          30
Ala Ala Ala Thr Val Leu Gln Thr His Gly Tyr Asp Gly Ser Ser Met
35          40          45
Asp Arg Val Ala Ser Gln Ala Gly Met Ser Lys Lys Thr Val Tyr Gln
50          55          60
Met Phe Pro Ser Lys Lys Ile Leu Phe Thr Lys Leu Leu Glu Asp Arg
65          70          75          80
Leu Phe Ser Ile Glu Trp Pro Glu Glu Lys Ile Cys Glu Asp Pro Glu
85          90          95
Glu His Leu Tyr Ser Leu Leu Ile Ala Ile Ala Gln Thr Ile Leu Arg
100         105         110
Pro Asp Arg Val Cys Leu Leu Arg Ile Leu Thr Val Glu His Lys Ser
115         120         125
Glu Glu Met Arg His Ile Phe Ser Asp Ile Leu Gln Gly His Thr Glu
130         135         140
Asp Asn Leu Thr Arg Trp Phe Ser Glu Gln Gln Asp Lys Gly Arg Tyr
145         150         155         160
His Ile Ser Asp Pro Ile Lys Tyr Ala Asp Ile Ile Phe Asn Met Thr
165         170         175
Val Gly Ser Leu Leu Leu Asp Arg Leu Phe Gly Leu Glu Lys Arg Pro
180         185         190
Val Glu Asp Asn Phe Arg Asp Ala Ile Ser Ile Phe Leu Arg Gly Ile
195         200         205
Arg Ile Asn Pro Glu Asn Glu
210         215

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<210> SEQ ID NO 17

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: PCR Primer

<400> SEQUENCE: 17

ccgtccttcc aattcgataa

20

<210> SEQ ID NO 18

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: PCR Primer

<400> SEQUENCE: 18

ccccaatatg accgaatcac

20

<210> SEQ ID NO 19

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: PCR Primer

<400> SEQUENCE: 19

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atcggcaatc atcaggaaag

20

<210> SEQ ID NO 20
 <211> LENGTH: 20
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: PCR Primer

<400> SEQUENCE: 20

ataccatgc cttcatctgc

20

We claim:

1. A microorganism of the genus *Zymomonas* comprising a genetic modification that increases the growth rate or biofuel production rate of the modified microorganism in the presence of a feedstock inhibitor compound relative to the growth rate or biofuel production rate of the unmodified microorganism wherein the genetic modification increases the expression or activity of a histidine kinase relative to the expression or activity level in the unmodified microorganism.

2. The microorganism of claim 1, wherein the genetic modification increases the expression or activity of ZMO1162 relative to the expression or activity level in the unmodified microorganism.

3. The microorganism of claim 1, wherein the genetic modification decreases the expression or activity of a functional sigma-54 modulation protein relative to the expression or activity level in the unmodified microorganism.

4. The microorganism of claim 1, wherein the genetic modification decreases the expression or activity of a functional protein encoded by ZMO0038 relative to the expression or activity level in the unmodified microorganism.

5. The microorganism of claim 1, wherein the genetic modification abolishes the function of a protein encoded by ZMO0038.

6. The microorganism of claim 1, wherein the microorganism is a bacterium.

7. The microorganism of claim 1, wherein the bacterium is a strain of *Zymomonas mobilis*.

15

8. The microorganism of claim 1, wherein the feedstock is corn stover.

9. The microorganism of claim 8, wherein the corn stover is pretreated with a dilute acid.

20 10. The microorganism of claim 1, wherein the feedstock inhibitor compound comprises furfural.

11. The microorganism of claim 1, wherein the biofuel is ethanol.

12. A method for producing a biofuel, comprising

25 a) culturing the microorganism of claim 1 with a feedstock under conditions whereby the microorganism ferments the feedstock into a biofuel; and

b) isolating the biofuel from the culture.

30 13. The method of claim 12, wherein the feedstock is lignocellulosic biomass.

14. The method of claim 13, wherein the lignocellulosic biomass has been pretreated with acid or enzymes to produce fermentable sugars.

35 15. The method of claim 12, wherein the feedstock is acid pretreated corn stover hydrolysate.

16. The method of claim 12, wherein the feedstock comprises fermentable sugars and at least one inhibitor compound.

40 17. The method of claim 16, wherein the at least one inhibitor compound is furfural.

18. The method of claim 12, wherein the biofuel is ethanol.

* * * * *